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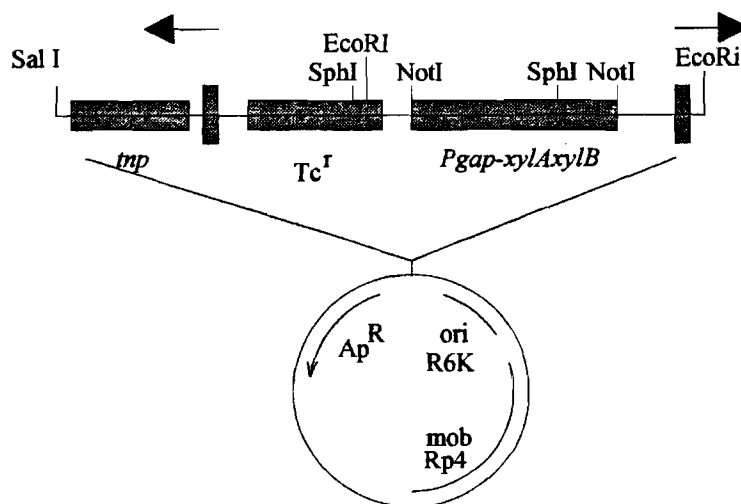
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(54) Title: STABLE *ZYMONAS MOBILIS* XYLOSE AND ARABINOSE FERMENTING STRAINS



(57) Abstract: The present invention briefly includes a transposon for stable insertion of foreign genes into a bacterial genome, comprising at least one operon having structural genes encoding enzymes selected from the group consisting of *xylAxB*, *araBAD* and *tal/tkt*, and at least one promoter for expression of the structural genes in the bacterium, a pair of inverted insertion sequences, the operons contained inside the insertion sequences, and a transposase gene located outside of the insertion sequences. A plasmid shuttle vector for transformation of foreign genes into a bacterial genome, comprising at least one operon having structural genes encoding enzymes selected from the group consisting of *xylAxB*, *araBAD* and *tal/tkt*, at least one promoter for expression of the structural genes in the bacterium, and at least two DNA fragments having homology with a gene in the bacterial genome to be transformed, is also provided. The transposon and shuttle vectors are useful in constructing significantly different *Zymomonas mobilis* strains, according to the present invention, which are useful in the conversion of the cellulose derived pentose sugars into fuels and chemicals, using traditional fermentation technology, because they are stable for expression in a non-selection medium.

Stable *Zymomonas mobilis* Xylose and Arabinose Fermenting Strains**Contractual Origin of the Invention:**

The United States Government has rights in this invention pursuant to Contract No. DE-AC36-99GO10337 between the United States Department of Energy and the Midwest Research Institute.

5 Technical Field

The present invention relates to the biological conversion of cellulosic substrates into fuels and chemicals, and in particular to recombinant *Zymomonas mobilis* strains which ferment xylose and arabinose, or both, into ethanol.

Background Art

10 Fermentation technology is useful for the conversion renewable biomass cellulose substrates into fuels and chemicals, such as ethanol. A typical substrate is comprised of 35-45% cellulose, 30-40% hemicellulose, and 15% lignin. The hydrolysis fraction contains glucose polymers, and the hemicellulose fraction contains mostly xylose. Arabinose is also a significant fermentable substrate found in biomass materials, such as switchgrass grass and corn fiber.

15 Thus, achieving a high rate of specific product formation and conversion efficiency in the fermentation of the pentose sugars is vital to the commercial production of fuels and chemicals from a renewable substrates.

Z. mobilis is widely reported for its ability to rapidly and efficiently convert glucose substrates into ethanol, at a low pH, in an anaerobic culture, and in a medium which contains the

20 inhibitory compounds typically associated with a lignocellulose-hydrolysate. A distinct disadvantage in the use of *Z. mobilis* is, however, that it does not ferment pentose sugars. To overcome this disadvantage, the prior art has focused on recombinant *Z. mobilis* strains which ferment a mixture of glucose, and xylose or arabinose, or both, using exogenous genes which catalyze the metabolism of xylose and arabinose. These strains, and the cloning vectors, are

25 based on the use of multiple-copy plasmids having antibiotic resistance markers.

US Pat. No. 5,514,583 discloses a transformed *Z. mobilis* xylose fermenting strain (CP4/pZB4 and pZB5) having exogenous genes, and plasmid vectors (pZB4 and pZB5) encoding xylose isomerase, xylulokinase, transaldolase and transketolase, and further comprising at least one promoter (*Pgap* and *Peno*) recognized by *Zymomonas* which regulates the expression of at

source, and fermenting xylose to ethanol at about 88% of the maximum theoretic yield. The Patent claims an integrated strain.

US Pat. Nos. 5,712,133 and 5,726,053 disclose, *inter alia*, *Z. mobilis* arabinose fermenting transformants (39676/pZB 206), containing exogenous genes that encode L-arabinose isomerase, L-ribulokinase and L-ribulose-5-phosphate-4-epimerase, transaldolase and transketolase which impart arabinose to ethanol fermentation capability. The plasmid vector (pZB 206) and a process of using the transformants for the fermentation of a glucose and arabinose containing substrate is also disclosed. The Patent claims integration of the exogenous genes into the host genome.

US Pat. No. 5,843,760 discloses a *Z. mobilis* xylose and arabinose fermenting transformant (206C/pZB301) containing exogenous genes encoding xylose isomerase, xylulokinase, L-arabinose isomerase, L-ribulokinase, L-ribulose-5-phosphate 4-epimerase, transaldolase and transketolase, and further comprising at least one promoter recognized by *Zymomonas* which regulates the expression of at least one of said genes, wherein said microorganism is capable of growing on arabinose and/or xylose, alone or in combination, as the carbon source and fermenting said arabinose and xylose to ethanol. The process of using the transformants together with the plasmid vectors (pZB301, pZB401, pZB402, and pZB 403) is also disclosed. This Patent claims integration of the exogenous genes into the host genome.

Although hybrid plasmids may be readily maintained in *Z. mobilis* when cultivated in mono-culture under controlled conditions, they frequently become unstable when the host organism is grown in the absence of selection pressure for plasmid maintenance, i.e., in the presence of antibiotics. For example, the exogenous genes in the above referenced strains are capable of stable expression for about forty generations. Instability may be exacerbated when *Z. mobilis* has to compete with other organisms in a mixed culture, such as a cellulose simultaneous-saccharification-fermentation process. In addition, antibiotic resistance markers are generally perceived as undesirable for industrial application, such as the large-scale production of ethanol. Thus, it is preferable to insert the cloned genes into the *Z. mobilis* genome, where they are maintained at a low, natural copy number, and are thus not over-expressed, and where, at least theoretically, they should be as stable as genomic DNA.

In *Escherichia coli*, the classical method for generating genomic inserts of foreign genes

state. Alternatively, genes can be inserted through homologous recombination, when bracketed with *E. coli* chromosomal sequences, or by transposition if the genes can be cloned in the permissive sites of a transposon. While transposition has been demonstrated in *Z. mobilis*, Pappas, K. M., *et al.*, (1997) Transposon mutagenesis and strain construction in *Zymomonas mobilis*, *Journal of Applied Microbiology*, Vol. 82, p.p. 379-388, it has been limited to mini M μ or Tn5 multiple transposition of random auxotrophy or antibiotic resistance phenotypes for genetic analysis, and in the case of the Tn5 derivatives the insertions are reportedly stable for only 5-15 generations. Pappas, K. M., *et seq.* P. 383, FIG. 1. Moreover, site-specific insertion through homologous recombination in *Z. mobilis* has not been demonstrated, and no bacteriophage has ever been isolated from *Zymomonas*.

Transposons Tn5 and Tn10 are well known and have been widely used for mutagenesis and insertion of cloned DNA into a variety of gram-negative bacteria. In Herrero, M., *et al.*, (1990) Transposon vectors containing non-antibiotic resistance selection markers for cloning and stable chromosomal insertion of foreign genes in gram-negative bacteria, *J. Bacteriol.* 172:6557-6567, a procedure is disclosed for cloning and stable insertion of foreign genes into the chromosome of gram-negative eubacteria by combining two sets of plasmids, (i) the transposition features of Tn10 and Tn5, (ii) the resistance to certain compounds, and (iii) the suicide delivery properties of the R6K-based plasmid pGP704. The resulting constructions contain unique *NotI* or *SfiI* sites internal to either the Tn10 or the Tn5 inverted repeats. These sites are used for cloning DNA fragments with the help of two additional specialized cloning plasmids, pUC18Not and pUC18Sfi. The newly derived constructions are maintained only in donor host strains that produce the R6K-specified π protein, which is an essential replication protein for R6K and plasmids derived therefrom. Donor plasmids containing hybrid transposons are transformed into a specialized λ pr i lysogenic *E. coli* strain, such as *E. coli* Sm10(λ pr i), with a chromosomally integrated RP4 that provided broad-host range conjugal transfer functions. Delivery of the donor plasmids into selected host bacteria is accomplished through mating with the target strain. Transposition of the hybrid transposon from the delivered suicide plasmid to a replicon in the target is mediated by the cognate transposase encoded on the plasmid at a site external to the transposon. Since the transposase function is not maintained in target cell, such cells are immune to further transposition rounds. Multiple insertions in the same strain are

Further disclosed in Herrero, M. *et al.*, 1990, Mini-Tn5 Transposon Derivatives for Insertion Mutagenesis Promoter Probing, and Genomic Insertion of Cloned DNA in Gram-Negative Eubacteria, *Journal of Bacteriol.* Vol 172, No. 11, p. 6568-6572, is the construction of a collection of Tn5-derived minitransposons, such as Tn5Tc, that enables the introduction of foreign DNA fragments into the chromosome of a variety of gram-negative bacteria. The minitransposons consist of genes specifying the resistance to kanamycin, and tetracycline as selection markers and a unique *NotI* cloning site flanked by 19-base-pair terminal repeat sequences of Tn5. The transposons are located on a R6K-based suicide delivery plasmid that provides the IS50_R transposase *tnp* gene in *cis* but external to the mobile element and whose conjugal transfer to recipients is mediated by RP4 mobilization functions in the donor. Therefore, insertions produced by these elements are generally more stable because of the absence of transposase-mediated secondary transpositions, deletions, and inversions. See also, Berg *et al.*, (1989) Transposable elements and the genetic engineering of bacteria, p.p. 879-926, in D.E. Berg, *Mobile DNA*, American Society for Microbiology, Washington, DC. Very stable insertions can in this way be obtained with elements derived, for instance also from Tn10. Way, J.C. *et al.*, (1984) New Tn10 derivatives for transposon mutagenesis and for construction of *lacZ* operon fusions by transposition. *Gene* 32: 369-379.

The structure of mini-Tn5Tc, Herrero, *et seq.*, p. 6569, is disclosed for use for insertion mutagenesis or as a transposon vector for the cloning of DNA fragments flanked by *NotI* sites (readily isolated by cloning DNA fragments first into the pUC18 derivatives pUC18Not and pUC18Not). The Mini-Tn5Tc element is constructed, *in vitro*, using standard recombinant DNA techniques. Maniatis, T., *et al.*, (1989) *Molecular cloning: a laboratory manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. The determinant for tetracycline (Tc) resistance is obtained as an *EcoRI* fragment from plasmids bearing them as an interposon. Fellay, R., *et al.* (1987) Interposon mutagenesis of soil and water bacteria: a family of DNA fragments designed for *in vitro* insertion mutagenesis of Gram-negative bacteria, *Gene* 52: 147-154. This fragments is subsequently cloned into the single *EcoRI* site of pUC18Sfi, excised as an *SfiI* fragment, and inserted between the Tn5 19-base pair termini in pUT so that the mobile unit is present in all cases as an *XbaI-EcoRI* (partial) portion of the delivery plasmid. The resulting element is mini-Tn5Tc.

Tn10-based transposon vector delivery systems are described in Herrero. M., *et seq.* 172:6557-6567. Phage λ , a derivative λ RP167, carries a 5.1-kb *EcoRI* insert containing the mini-Tn10Km element and the transposase gene of IS10_R is located outside the inverted repeats of the mobile element and downstream of the *pTac* promoter. To obtain a transposon delivery
5 plasmid with a host-independent regulation of its transposition, the *EcoRI* insert fragment is ligated to pBOR8, a derivative of pGP704 containing the *lacI^q* gene from plasmid pMJR1560. This plasmid is unable to replicate in host strains devoid of the R6K-specified π protein product of the *pir* gene. pGP704 contains the conjugal transfer origin (*oriT* sequence) of the RP4
10 plasmid and can therefore be transferred to gram-negative bacteria when provided in *trans* with mobilization (Mob) functions. The *MluI* fragment internal to the inverted repeats containing the original-specified π protein product of the original kanamycin resistance gene of the mini-Tn10 is replaced by a fragment containing a *SfiI*-Ptt cassette, appropriately modified by the addition of the *NotI* site and *MluI* adapters, which produced the pLODPtt. This construction has unique *SfiI*, *NotI*, and *XbaI* cloning sites between the mini-Tn10 inverted repeats. The Ptt resistance marker
15 (Ptt^r) of pLOFPtt is exchanged by kanamycin resistance to produce plasmid pLOFKm.

In view of the foregoing, a need exists for the construction of stable recombinant *Z. mobilis* strains which are capable of fermenting xylose and arabinose, or both, to ethanol through the generation of stable genomic inserts which encode the enzymes which are necessary for xylose and arabinose catabolism. The strains should be free of antibiotic resistance and stable
20 for more than 40 generations in a non-selection media. It is also desirable for the strains to demonstrate a high specific rate of product formation at close to maximum theoretical product yield.

Disclosure of Invention

It is an object of the present invention to provide transposable element and plasmid
25 vectors useful for the stable integration of foreign structural genes, encoding enzymes selected from the group consisting of *xylA**xylB*, *tal/tkt*, and *araBAD* and at least one regulator gene for induction of the structural genes, into the *Z. mobilis* genome.

It is a further object of the invention to provide significantly different *Z. mobilis* strains capable of stable expression of the structural genes in a non-selection medium.

It is yet another object of the invention to provide significantly different *Z. mobilis* strains, having stable expression of the structural genes, but which are characterized by a high rate of specific product formation and conversion efficiency, when used as a bio-catalyst in a cellulose hydrolysate reaction mixture.

5 To overcome the problems associated with the related art and in accordance with the purpose of the invention, as embodied and broadly described herein, the present invention briefly includes: a transposon for stable insertion of foreign genes into a bacterial genome, including: at least one operon having structural genes encoding enzymes selected from the group consisting of *xylA**xylB*, *araBAD* and *tal/tkt*, and at least one promoter for expression of the structural genes in
10 the bacterium, a pair of inverted insertion sequences, the operons contained inside the insertion sequences, and a transposase gene located outside of the insertion sequences; a plasmid shuttle vector for transformation of foreign genes into a bacterial genome, including: at least one operon having structural genes encoding enzymes selected from the group consisting of *xylA**xylB*, *araBAD* and *tal/tkt*, at least one promoter for expression of the structural genes in the bacterium,
15 and at least two DNA fragments having homology with a gene in the bacterial genome to be transformed.

The transposon and shuttle vectors are useful in constructing significantly different *Zymomonas mobilis* strains, according to the present invention, which are useful in the conversion of the cellulose derived pentose sugars into fuels and chemicals, using traditional
20 fermentation technology, because they are stable for expression in a non-selection medium.

Additional advantages of the present invention will be set forth in part in the description that follows and in part will be obvious for that description or can be learned from practice of the invention. The advantages of the invention can be realized and obtained by the method particularly pointed out in the appended claims.

25 **Brief Description of Drawings**

The accompanying drawing, which are incorporated in and which constitute a part of the specification, illustrate at least one embodiment of the invention and, together with the description, explain the principles of the invention.

Figure 1 is a plasmid map of Mini-Tn5 Tc in pGP704 containing the xylose assimilation
30 operon according to the present invention.

Figure 2 is a series of plasmid maps illustrating the mini-Tn5 series constructs, according to the present invention.

Figure 3 is an illustration of the series of constructs resulting in the plasmid map of pUC $\text{tal} \text{tk} \text{tSfi}$.

Figure 4 is the results of the Southern analysis *tal/tkt-xylA_{xylB}* *Z. mobilis* transconjugates with Tal probe. C is the control plasmid mini Tn5 *tal/tkt-xylA_{xylB}*. λ H is the DNA size marker.

Figure 5 is the results of the Southern analysis of *tal/tkt-xylA_{xylB}* *Z. mobilis* transconjugates with Tnp probe. C is the control plasmid mini-Tn5 *tal/tkt-xylA_{xylB}*. λ H is the DNA size marker.

Figure 6 is a graph of the enzymatic activities for several isolates of the stable xylose fermenting *Z. mobilis* strain according to the present invention.

Figure 7 illustrates graphs of the fermentation profiles for four of the isolates (nos. 21, 22 and 5) of Figure 6 and their performance in relation to the plasmid bearing strains 39673/pZB4 and BC1/pZB4L.

Figure 8 is a graphic representation which illustrates the stability of the stable xylose fermenting *Z. mobilis* strains C25 and D95 according to the present invention. The graph shows the stability of the plasmid-bearing and genomic integrated xylose-fermenting strains, using the ethanol process yield and xylose utilization parameters as indicators. Strains C25 and D95 of the present invention remained stable for more than 90 generations. The fermentation medium comprised RM with 1% glucose and 5% xylose and the temperature was constant at 30°C.

Figure 9 illustrates the biomass concentration at optical density (OD₆₀₀), the xylose utilization as a function of time, ethanol production as a function of time, and process yield compared to the percent xylose utilization for batch fermentation of the genomic integrated xylose-fermenting strains, C25 and D95, in a RM medium containing 4.5% glucose, and 4.5% xylose at pH 5.0 and pH 5.5 at 30°C, according to the present invention.

Figure 10 is a map of the integrative plasmid pZB 1862-ldhL-ara. The *araBAD* is inserted in the NotI site of *ldhL* disrupting *ldh*. The construction is based on the replicative plasmid pZB 1862 of *Z. mobilis*.

Figure 11 is the plasmid map of Tn10G. IS10_R is the transposase gene. IR is the inverted repeat sequence of the transposon. *AraBAD* was inserted between two the two inverted

Figure 12 shows the Southern analysis of the genomic integrated xylose/arabinose-fermenting *Z. mobilis* strains from homologous recombination using DIG-*ara* and DIG-*ldh* probes. AX1, 13, 23, 101, 104, and 107 are *araBAD* integrants. C25 is the host control. pZB1862-*ldhL-ara* is a plasmid control isolated from DH5 α . λ /H is a molecular weight marker: 23, 9.4, 6.6 4.3, 2.3 and 2.0 kb.

Figure 13 represents a Southern analysis of the genomic integrated xylose/arabinose-fermenting *Zymomonas* strains from transposon integration using DIG-*tnp* and DIG-*ara* probes. G5,6,11,15,17,14 and 19 are *araBAD* integrants. C25 is the host control. Tn10G is the plasmid control. λ H is a molecular weight marker: 23,9.4,6.6,4.3,2.3 and 2.0 kb. Figure 13 (a) is the *tnp* *Pst*I digestion and Figure 13 (b) is the probe *ara* *Pst*I digestion.

Figure 14 represents bar graphs of the enzymatic activities of the transketolase, transaldolase, xylose isomerase and xylulokinase of the genomic integrates strains. 206C/pZB301 is a plasmid control. 206C is a host control. C25 is the xylose-fermenting integrant. G8 is the xylose/arabinose fermenting integrant from Tn10 transposition. AX1 and AX101 are the xylose/arabinose fermenting integrants from homologous recombination.

Figure 15 represents bar graph results of the enzymatic activities of L-arabinose isomerase, L-ribulokinase and L-ribulose-5-phosphate-4 epimerase of genomic integrated strains. 206C/pZB301 is a plasmid control. 206C is a host control. C25 is the xylose-fermenting integrant. G8 is the xylose/arabinose-fermenting integrant from Tn10 transposition. AX1 and AX101 are the xylose/arabinose-fermenting integrants from homologous recombination.

Figure 16 represents a bar graph result of the ethanol process yields of the genomic integrated xylose and arabinose-fermenting *Zymomonas* strains on RMGXA (1:2:2%) at T=30° C, without pH control. These strains were inoculated from cultures at various generations on non-selective media.

Figure 17 represents a bar graph results of the xylose and arabinose utilization of the genomic integrated xylose and arabinose-fermenting *Zymomonas* strains on RM containing 1% glucose, 2% xylose and 2% arabinose at 30°C with pH control. These strains were inoculated from cultures at various generations on non-selective media.

Figure 18 is a line graph representation of the fermentation performance of the genomic integrated xylose and arabinose-fermenting *Zymomonas* strains in RM containing 4% glucose,

Detailed Description of Drawings

Unless specifically defined otherwise, all technical or scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All US Patents are incorporated by reference as though fully set forth herein.

Reference now will be made in detail to the presently preferred embodiments of the invention, examples of which are illustrated in the accompanying drawings. For the examples described below, "plasmid-bearing strains" refers or relates to those strains and vectors described in the US Patents identified in the Description of the Related Art. "*Z. mobilis* genome, or genomic" means the genes which, *in toto*, specify all the expressed and potentially expressible features associated with a given *Z. mobilis*. C25 refers to *Zymomonas mobilis* Patent Deposit Designation PTA-1799; AX refers to *Zymomonas mobilis* Patent Deposit Designation PTA-1797; G8 refers to *Zymomonas mobilis* Patent Deposit Designation PTA-1796 mini-*Tn5-tal/tkt-xylA*; *xylB* refers to *Escherichia coli*: DH5 α (pZb 1862-*IdhL*-ara) Patent Deposit Designation PTA-1798; and C25 refers to *Zymomonas mobilis* Patent Deposit Designation PTA-1799. All of the above are on deposit with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, received 2 May 2000, in accordance with the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure and have been accepted.

Examples

Strains, Plasmids, and Media.

E. coli bacterial strains CC118 λ (*pir*), CC118 λ (*pir*) (mini-*tn5*Tc), SM10 λ (*pir*), and plasmids pUC19, pLOF/Km, pUC18sf, pUT/Tc containing minitransposon Tn5, Tn 10 and pUC18Not were obtained from Dr. K. Timmis, GBF - Gesellschaft Fur Biotechnologische Forschung mbH, Mascheroder weg 1 D - 38124 Braunschweig, Federal Republic of Germany. *E. coli* DH5 α was used as a host for the construction of the plasmids. *E. coli* SM10 λ *pir* was used as donor strain in mating experiments. Strains of *Z. mobilis* ATCC 39676 and its derivative, 206C (US Pat. No. 5,843,760) were used as recipients in accordance with the

E. coli strains were cultured in LB medium at 37° C. *Z. mobilis* strains were maintained anaerobically in RM (10 g/L yeast extract, 2 g/L KH₂PO₄) supplemented with 20g/L glucose, D-xylose or L-arabinose, unless otherwise specified. All strains containing plasmids were grown in the presence of tetracycline (Tc) ((10µg/ml in liquid *Z. mobilis*, and *E. coli*; 20 µg/ml in agar for *Z. mobilis*; and 15 µg/ml in agar, or ampicillin (Ap), 100 µg/ml for *E. coli*)). For regeneration and selection of *Z. mobilis* transformants or transconjugates, mating plates ((10 g/L yeast extract, 5 g/L tryptone, 2.5 g/L (NH₄)₂SO₄, 0.2 g/L K₂HPO₄ and 50 g/L sugar)) supplemented with tetracycline or nalidixic acid (20 µg/ml) were used. All agar plates were made with 15 g/L agar.

Recombinant DNA techniques.

Plasmid DNA isolation, restriction endonuclease digestion, ligation and transformation, agarose electrophoresis and other recombinant DNA techniques were carried out in accordance with published protocols, Sambrook *et al.*, (1989) *Molecular cloning: a laboratory manual*, Cold Spring Harbor laboratory press, Cold Spring Harbor, NY, or the respective reagent manufacture's instructions, were specified, and are well known in the art. Genomic DNA of *Z. mobilis* was extracted using three-milliliters of overnight cells resuspended in 250 ml of 50 mM Tris-50 mM EDTA buffer. The cells were treated with lysozyme at 37°C for 30 min and 100 ml of 5% SDS solution and RNAase (final concentration equal to 20 ng/ml) were then added and the mixture was incubated for an additional 30 min. A phenol/chloroform extraction was performed twice, to remove the proteins. Genomic DNA was recovered by ethanol precipitation.

Conjugation and transformation.

Plasmids were transferred from the donor strains *E. coli* SM10λpir or S17-1 into *Z. mobilis* strains by conjugation with a filter mating technique (Conway et al., 1987). Plasmid DNAs were transformed into either *Z. mobilis* or *E. coli* cells by electroporation (Zhang et al., 1995)).

Southern Blot analysis.

DNA was transferred onto a nylon membrane using a Stratagene Posi Blot pressure blotter. DNA probes Tc, xylB, Tnp, and Tal were digoxigenin-UTP labeled by Polymerase

Tc: 5'-TTGCTAACGCAGTCAGGC-3' SEQ. ID NO. 1.
 5'-GAATCCGTTAGCGAGGTG-3' SEQ. ID NO. 2.
 xylB 5'-TATGGGTTCAGCGGCATGAG-3' SEQ. ID NO. 3.
 5'-ATGGGCATGAGATCCATAGCC-3' SEQ. ID NO. 4.
 5 Tnp 5'-TCCTAACATGGTAACGTTC-3' SEQ. ID NO. 5.
 5'-CCAACCTTACCAGAGGGC-3' SEQ. ID NO. 6.
 Tal: 5'-CGTCTAAAAGATTTTAAGAAAGGTTTCGATATGACGGACAA
 ATTGACC-3' SEQ. ID NO. 7.
 5'-CATTTTGACTCCAGATCTAGATTACAGCAGATCGCCGATC
 10 ATTTTTTCC-3' SEQ ID NO. 8.

Prehybridization and hybridization were performed according to established protocols described in the Boehringer Mannheim hybridization kit.

EXAMPLE I

15 The following example illustrates the construction of Mini-Tn5Tc containing genes encoding the xylose assimilation enzymes and the conjugal transfer of this construct into *Z. mobilis* 206C and ATCC 39676. Mini-Tn5Tc containing genes encoding the xylose assimilation enzymes was constructed by inserting a *Pgap-xylA**xylB* operon into the unique *NotI* site of Mini-Tn5Tc contained in plasmid pGP704. See, Figure 1. The *Pgap-xylA**xylB* operons, were taken
 20 from plasmid pZB4 or pZB5, US Pat. Nos. 5,712,133 and 5,726,053. The resulting plasmids, designated Mini-Tn5Tc *xylA/xylB*(X4) and Mini-Tn5Tc *xylA**xylB* (X5), were transformed into the donor strain *E. coli* SM10 λ *pir* by electroporation and mated with either *Z. mobilis* ATCC 39676 and 206C strains. *Z. mobilis* 206C is disclosed in US Pat. No. 5,843,760 which is incorporated herein by reference. Nine *Zymomonas* Tc^r transconjugates were obtained from both
 25 SM10 λ *pir* donors containing Mini-Tn5Tc*xylA**xylB* (X4) and Mini-Tn5 Tc*xylA**xylB* (X5) by selection on media containing Tc and nalidixic acid. See, Figure 2(b).

Genomic and plasmid DNA from the nine *Z. mobilis* Tc^r transconjugates was then subjected to Southern blot analyses. Genomic and plasmid DNA from the transconjugates was digested with *SphI*, which cuts in the hybrid transposon and in the xylose operon, and the blots
 30 were then hybridized to either a Tc probe, a XylB probe, or a transposase Tnp probe. From the autoradiograph it was determined that: (1) the xylose operon *Pgap-xylA**xylB* had been inserted

into the *Zymomonas* genome, along with Tc^r gene; (2) only a single insertion had occurred for each of the transconjugates; (3) the insertions were each at a distinct location in the genome; (4) the Tc^r gene and XylB were not present the plasmid fraction; and (5) the *tnp* transposase gene was not present in transconjugates.

5 Enzymatic analysis of the *Zymomonas* Tc^r *Pgap-xylA**xylB* Transconjugates was made in order to confirm the expression of xylose isomerase (XI) and xylulokinase (XK) in the *Zymomonas* Tc^r *Pgap-xylA**xylB* transconjugates. This analysis revealed that the enzymatic levels of xylose isomerase for the all the transconjugates was about one-half that of their plasmid counterparts. Similarly, about one-half of the xylulokinase activities of the plasmid-bearing
10 strains was observed in the integrants. Both XI and XK activities, expressed from a single copy of the genes, in the *Zymomonas* genome, were considerably higher than was expected, when compared to that of the 10 copies per cell found in a plasmid-bearing strains.

EXAMPLE II (C25)

15 This example shows that to enhance the genetic stability of the recombinant *Z. Mobilis*, in the absence of antibiotic selection, the xylose assimilation genes *xylA* and *xylB*, encoding xylose isomerase and xylulokinase, and pentose phosphate pathway genes, *talB* and *tktA*, encoding transaldolase and transketolase, were introduced into the *Z. mobilis* genome, using mini-Tn5. Two operons containing *Pgap-xylA/xylB* and *Peno-talB/tktA* were assembled in mini-Tn5 and the
20 resulting plasmid was conjugated into *Z. mobilis*. With the help of the transposase located outside of the mini-Tn5 cassette, single copies of the *Pgap-xylA**xylB* and *Peno-talB/tktA* were inserted into the *Z. mobilis* genome, as shown by Southern hybridization. Enzymatic analysis of xylose isomerase, xylulokinase, transaldolase and transaldolase indicated that all the genes were coordinately expressed and that the integrated strains produced about 30-70% of the enzymatic
25 activities of the plasmid-bearing strains. These enzymatic levels were sufficient for the organism to grow and ferment xylose to ethanol.

To facilitate the cloning process, the *Bgl*II fragment containing the operon *Peno-talB/tktA* was inserted into the *Bam*HI site of a newly constructed auxiliary plasmid, pUSCfiMCS as shown in Figure 3. The auxiliary plasmid, pUSCfiMCS, was constructed by inserting a *Eco*R I-
30 *Hind* III fragment containing the multicloning sites from pUC19 into pUCSfi. PUC*tal**tk*t was

Referring now to Figure 2, the *Peno-talB/tktA* was then excised, from pUCtal_{tk}tS_{fi}, as a *Sfi*I fragment and was used to clone into mini-tn5-Tc-*xylA_{xylB}*. As shown in the Figure, the Tc^r gene is flanked by *Sfi*I sites on the Tn5-Tc-*xylA_{xylB}* cassette. Mini-tn5-Tc-*xylA_{xylB}* was partially and completely digested with *Sfi* I and ligated to the *Peno-talB/tktA*S_{fi} fragment, as shown in Figure 2(c). The partial digestion yielded a plasmid containing the Tc^r gene, designated as mini-tn5- Tc *tal/tkt-xylA_{xylB}* ((Fig. 2(c)), while complete digestion yielded a plasmid, according to the invention herein, without the Tc^r gene, designated as miniTn5-*tal/tkt-xylA_{xylB}*. See Figure 2(d).

Both plasmids were transformed into the donor strain *E. coli*, S17-1 and mated with *Z. mobilis* 206C. The resulting transconjugates were selected on mating media containing glucose, Tc, and nalidixic acid for miniTn5-*tal/tkt-xylA_{xylB}*-Tc. For mini-tn5-*tal/tkt-xylA_{xylB}*, the transconjugates were directly selected on mating media, containing xylose and nalidixic acid. A number of Tc^r transconjugates (glucose-grown) were obtained for mini-tn5 *tal/tkt-xylA_{xylB}*-Tc. Several xylose-grown transconjugates were obtained for mini-tn5-*tal/tkt-xylA_{xylB}*.

Preliminary batch cultures were tested statically, at 30° C without pH control in bottles with 80 ml RM containing 2% xylose for their fermentation dynamics. Colonies, taken from RM+2% xylose plates were cultured in an RM 2% xylose medium overnight at 20° C until the culture had reached the stationary growth phase (optical density₆₀₀ = 0.1 at 500 nm), were used as the inoculum. Xylose and ethanol were analyzed using a Hewlett-Packard 1090L HPLC equipped with an HP 1047 A refractive index detector and a Biorad HPX-87H organic acid analysis column operating at 65° C, with a 0.01 N sulfuric acid mobile phase flow rate of 0.6 ml/min. The ethanol yield was calculated using either the weight of sugar fermented or the total available sugar in the medium. The maximum theoretical yield was based on 0.51 g ethanol/ g xylose.

Southern bolt analysis of genomic and plasmid DNA samples from the *Z. mobilis* transconjugates was made in order to investigate whether transposition of the mini-tn5 *tal/tkt-xylA_{xylB}* cassette had occurred. Genomic and plasmid DNAs prepared from four transconjugates of mini-tn5 *tal/tkt-xylA_{xylB}* were digested with *Sph*I, which cuts twice within the cassette yielding one fragment with Tal probe homology. The blots were then hybridized to either Tal probe or Tnp probe. The autoradiograph in Fig. 4 shows that one unique band greater than 4kb (the size of *Peno-talB/tktA*), which is adjacent to *Z. mobilis* DNA, was detected from

all the genomic DNA preparations when hybridized with Tal probe. Three of the samples (nos. 22,23, and 24 possibly siblings) also showed a band in the plasmid fraction, suggesting that the integration had occurred in the native plasmid. Clearly integration had occurred in the *Z. mobilis* genome for sample no. 21, and only one copy was inserted. Hybridization of genomic and plasmid DNA samples from these transconjugates with a Tnp probe (Fig. 5) revealed a lack of homology between the sample DNA's and Tnp probe. These results suggested that the xylose assimilation and pentose phosphate pathway genes, along with Tc^r gene, had been transposed into the *Z. mobilis* genome, and that only a single insertion occurred in each of the transconjugates, and the insertions were at distinct locations in the genome.

Xylose isomerase, xylulokinase, transaldolase and transketolase activities were measured as previously described in (Zhang et al., 1995), for the *Z. mobilis* transconjugates. As set forth above, it had been observed that expression of a single *Pgap-xyIAxylB* copy on the genome was about one-half that of the XI and XK enzymatic yielded for the plasmids-bearing strains. However, when enzymatic analysis was done to confirm whether transaldolase (TAL) and transketolase (TKT) had been expressed in the *Zymomonas tal/tkt-xyIAxylB*-Tc and *tal/tkt-xyIAxylB* transconjugates, as shown in Figure 6, it was revealed that the enzymatic levels of TAL, for the all the transconjugates (nos. 4,5,17,18,21,23, and 24), was about 50-70% that of their plasmid counterparts. About 30-70% of the TKT activities of the plasmid-bearing strains was observed in the integrants. While the plasmid integrants had slightly elevated TAL and TKT activities, both TAL and TKT activities, expressed from a single copy of the genes in the *Zymomonas* genome, were considerably higher than was expected when compared to that of the 10 copies per cell found on a plasmid- bearing strain.

All four of the *tal/tkt-xyIAxylB* *Zymomonas* integrants (nos. 21, 22, 5, and 11) were able to grow on xylose. Preliminary fermentation studies for these integrants was then made using a 2% xylose substrate, at 30° C. The fermentation profiles, for these integrants, is shown in Figure 7. In the Figure, the growth and sugar utilization rates of *Z. mobilis* integrant no. 21 was slower than that of the plasmid bearing strain 39676/pZB4. However, most of the *Z. mobilis* integrants (nos. 22,5, and 11) were comparable to the plasmid-bearing strains. All the integrants produced ethanol from xylose, at 92% of the maximum theoretical product yield.

Stability of these genomic integrated strains and three plasmid bearing strains was

transferred about every 10 generations daily. At every 40 generations, the cells were used to inoculate a flask of RM media containing 1% glucose, and 5% xylose in order to measure their ability to ferment xylose to ethanol. Ethanol process yields and xylose utilization rates were used as the milestones for stability. Two of the genomic integrated strains demonstrated stability
5 for more than 90 (C25 and D95) generations, while the plasmid-bearing strains (206/pZB4, 206/pZB4L and BC1pZB4L) were stable for about 40 generations. See, Figure 8.

The fermentation performance of strains C25 and D95 was analyzed in an RM medium containing a different concentrations of total glucose and xylose (1% glucose and 5% xylose; 3% glucose and 3% xylose; and 4.5% glucose and 4.5% xylose) under pH controlled conditions. As
10 shown in the Figure, strain C25 demonstrated much better xylose utilization and ethanol process yields at both pH 5, and pH 5.5 in RM containing 4.5% glucose and 4.5% xylose than D95. Consequently, in the subsequent examples the three arabinose assimilating genes (*araBAD*) were integrated into the C25 genome.

15 EXAMPLE III (AX)

The following example demonstrates the introduction of the arabinose assimilation enzymes in the genome of C25 through homologous recombination via *ldh* and transposition using mini-transposon Tn10. Plasmid pZB1862-*ldhL*-*ara*, described below, was used to transform *Z. mobilis* or *E. coli* by electroporation. Transformants were selected on mating plates
20 supplemented with glucose and tetracycline. Tc^r colonies were further confirmed to be Ara⁺Xyl⁻ by growth on RM supplemented with xylose or arabinose (RMS and RMA). Plasmid Tn10G, also described below, was transferred from an *E. coli* SM10 λ *pir* donor to *Z. mobilis* C25 by conjugation with a filter mating technique (Conway *et al.*, 1987). The resulting transconjugates were selected on mating plates containing arabinose.

25 A. Construction of pZB1862-*ldhL*-*ara* and integration in C25 using homologous recombination.

Previous attempts to integrate *araBAD* in the *Zymomonas* genome, using a 1-kb *ldh* fragment as the homologous region, did not succeed. In order to increase the recombination frequency, a larger homology region was used. A 2.5-kb DNA fragment, which includes *ldh* and
30 the flanking region was amplified using *Pfu* PCR and DNA from *Z. mobilis* ATCC 39676, US

mobilis CP4, published in Yamano I., (1993) *Journal of Bacteriology*, Vol. 175, 3926-3933.

Although a 2.5-kb fragment was expected from PCR, according to the published sequence, a 3.4-kb fragment was obtained instead. After digesting the 3.4-kb fragment with *Bam*HI, two fragments (2.5 and 0.9 kb) were obtained. Both fragments were tested by PCR, using primers designed to anneal to only the *ldh*. The 2.5-kb fragment produced a PCR product of the correct size, whereas the 0.9-kb fragment did not, indicating that the former contained the *ldh* sequence. Therefore, the 2.5-kb *Bam*HI fragment (designated *ldhL*) was cloned and used as the homologous region for gene integration into C25.

The *ldhL* fragment and digoxigenin (DIG)-labeled *ldh*, *ara*, and *tnp* probes were amplified by PCR using either Pfu (Stratagene, La Jolla, CA) or Taq DNA polymerase (Qiagen, Valencia, CA). DIG-UTP was purchased from Boehringer Mannheim, Indianapolis, IN. A I probe was used to probe for *IS10_R*, the transposase gene of *Tn10*. PCR products for *ldhL*, *ldh*, *ara*, and *tnp* are 2.5, 1, 1.4 and 0.8 kb, respectively. The following primer sequences were used:

ldhL: 5'-TCGCGGATCCTCTATCCCTTATTTTCTATCCCCATCACCTCGG-3'

SEQ. ID NO. 9.

5'-TCGCGGATCCGCGGCTGACATACATCTTGCGAATATAGGG-3'

SEQ. ID NO. 10.

DIG-*ldh*: 5'-TCGCGGATCCGTCTATGCGCGTCGCAATATTCAGTTCC-3'

SEQ. ID NO. 11.

5'-TCGCGGATCCGTGCTTGTCTATTAAACAAGCGCATCCGGC-3'

SEQ. ID NO. 12.

DIG-*ara*: 5'-CTAACATGTTGACTCCTTCTCTAGACTTAGCG-3' SEQ. ID NO. 13.

5'-GTTGAAACCGCTGGGCACACGC-3' SEQ. ID NO. 14.

DIG-*tnp*: 5'-CGCACTACACGGTCGTTCTGTTAC-3' SEQ. ID NO. 15.

5'-GGTTGCAGCCACGAGTAAGTCTTC-3' SEQ. ID NO. 16.

For cloning purposes, a *Not*I site was introduced in *ldhL* by insertion of an oligonucleotide 5'-CATGCGGGCCGCC-3' at *Nco*I site, which is located in the middle of the *ldh* gene. The new *Not*I site was approximately 1.4 and 1.1 kb from either end of *ldhL*. A *Bam*HI fragment of *ldhL* (2.5 kb) containing the *Not*I site was ligated into pZB1862 at a *Bcl*II site. Finally, a 4.4-kb *Pgap-araBAD*, isolated from pZB206 (US Pat. Nos. 5,712,133 and

5,726,053), was cloned into the *NotI* site, of *ldhL*, to form the integrative plasmid, pZB1862-*ldhL*-ara. See, Figure 10.

The *Pgap-araBAD* operon, containing the three arabinose-assimilating genes, was integrated into the *ldh* site in the C25 genome through homologous recombination. To integrate the *araBAD* genes into the genome of C25, pZB1862-*ldhL*-ara was constructed in *E. coli* DH5 α . The plasmid pZB1862-*ldhL*-ara was transferred into C25 by electroporation. The Tc resistant transformants were selected and tested for growth on arabinose. During propagation of the transformants, *Pgap-ara-BAD* could be integrated in the genome of C25 by the replacement of *ldhL* with the *ldhL*'-*araBAD*-*ldhL*' cassette (from the plasmid) through homologous recombination.

To enrich and isolate the integrants, plasmid curing was conducted for the transformants. Plasmid pZB1862-*ldhL*-ara will replicate in *Z. mobilis*. However, *Z. mobilis* tends to lose foreign plasmids at sub-optimal growth conditions (e.g. 37° C). Using this characteristic, curing of pZB1862-*ldhL*-ara was achieved by subculturing C25 transformants at 37° C in the absence of Tc for several transfers. Cultures from each transfer were constantly monitored for the loss of the plasmid. By the third transfer, 100% of the cells became Tc^s, indicating a loss of the plasmid. Cultures from the 3rd, 4th, 5th, and 6th transfers were inoculated in RM containing arabinose (RMA), at 30° C. to enrich the growth of potential *Pgap-araBAD* integrants. The enriched cells were transferred to RMG plates and replica-picked onto RMA, RMX, and RMGTc plates. Several integrants (AX) with the phenotype of Xyl⁺Ara⁺Tc^s were subjected to further analysis, as described below. These integrants were able to use either xylose or arabinose as a sole carbon source.

B. Construction of Tn10G and Conjugation into C25.

Mini-Tn5 was used for constructing C25 with *Peno-tal/tkt* and *Pgap-xylAB* operons. Although the transposase gene did not exist in C25, mini-Tn10 was used for the subsequent integration of *Pgap-araBAD* to avoid any possible incompatibility between the same transposons. Plasmid Tn10G (Fig.11) was constructed based on the Tn10-based delivery plasmid, pLOFKm. The Km^r gene was replaced by a *NotI* fragment of *Pgap-araBAD*, isolated from pZB206. Tn10G was constructed and maintained in *E. coli* C118. The plasmid was then transferred into the mating donor, *E. coli* SM10 λ pir for conjugation with *Z. mobilis*. Since

able to grow on mating plates, supplemented with arabinose. The *E. coli* SM10 λ *pir* donor was inhibited, in the plates, by the presence of nalidixic acid. Transconjugates appeared on mating/ara plates in 7 days. Colonies were replica-picked onto RMA and RMX to confirm their phenotypes. Eighty-six percent of the colonies picked were Xyl⁺Ara⁺. Twenty colonies from the pick-plates were cross-transferred to different plates (from xylose plates to arabinose plates or vice versa). Sixty percent of those colonies remained Xyl⁺Ara⁺. Twenty colonies were analyzed in a preliminary Southern hybridization (data not shown). Using the *tnp* probe, about 50% of the strains contained the transposase gene in the genome. Eight integrants were then subjected to detailed analysis by Southern hybridization.

Integration of *Pgap-araBAD* in *ldh* of C25 was confirmed by Southern hybridization, for the pZB1862-*ldhL-ara* integrants DNA using the DIG-labeled *ara* and *ldh* probes. See, Figure 12(a) and (b). There is only one *Pst*I site on pZB1862-*ldhL-ara* and it is located in *Pgap-araBAD*. Therefore, one hybridization band (12.9 kb) from the *Pst*I-digested plasmid was expected, using the *ara* probe. With *Pgap-araBAD* integrated in the genome two bands generated by the *Pst*I site in *Pgap-araBAD* and the adjunct *Pst*I sites on the genome located outside the *Pgap-araBAD* were expected. The results from Figure 13(a) clearly showed that two bands from the total DNA preparation hybridized with the *ara* probe and demonstrated integration of *Pgap-araBAD*. The lack of hybridization bands from plasmid DNA of integrants indicated that integration had occurred on the genome, rather than on native plasmids. To show that the *ldh* was disrupted by the *Pgap-araBAD* integration, the same DNA was transferred and hybridized with the *ldh* probe. As expected, the hybridization patterns for the integrants were exactly the same on both blots, except for C25, as shown in Figure 12(b). The total DNA from the host strain, C25, used for *Pgap-araBAD* integration, which has an intact *ldh*, showed only one band. The results confirmed that *araBAD* was integrated in *ldh* of C25.

Figures 13(a) and (b) show the Southern hybridization results using DIG-labeled *Tnp* and *ara* probes, respectively, for the eight *Pgap-araBAD* transposon integrants generated by *Tn10* transposition. DNA was digested with a *Pst*I restriction enzyme. *Pst*I cuts *Tn10G* into two fragments (7.7 and 5.9 kb) and only the 5.9-kb fragment carries the transposase gene (*IS10_R*). Both fragments hybridized with an *ara* probe. According to the blots, only G8, G11, G15 and GH17 were *ara*-positive and *tnp*-negative. Different band patterns indicated that *Pgap-araBAD*

to remain in the genome of the integrants, four strains (G5, G6, G14 and G19), out of the eight, contained the transposase gene. Furthermore, G14, and G19 contained the transposase gene on the plasmid. With an *ara* probe, two bands from the integrants were expected. However, only single bands were observed. To solve this ambiguity, PCR was conducted, for the integrants, using *ara* primers and it was confirmed that all eight integrants contained *Pgap-araBAD* in the genome (data not shown).

Xylose isomerase (XI), xylulokinase (XK), L-arabinose isomerase (L-AI), L-ribulokinase (L-RK), L-ribulose-5-P-4-epimerase (L-Repi), transketolase (TKT) and transaldolase (TAL) were assayed, using cell-free extracts of the *Z. mobilis* integrants and control strains, according to Zhang, *et al.*, 1995; and Deanda *et al.*, 1996, with minor modifications. Cell-free extracts were prepared by collecting the cultures at late-log phase (30°C, OD₆₀₀ approximately 1.2), washing once with sonication buffer (10 mM Tris-HCl, pH 7.6 10 mM MgCl₂) and sonicating. The cell debris was removed by centrifugation (14,000 rpm, 45 min 4°C). In the L-AI assay, the volumes of timed samples were scaled down by half (50µl), 70% H₂SO₄ (1.5 ml) and 0.12% carbazole (50µl). All of the tubes were maintained in a 25°C water bath, both before and after the addition of 70% H₂SO₄, until reading the absorbency. The samples were taken at 0,5,10, and 20 min during the reaction.

Although the integrants, from both homologous recombination and transposon integration, were able to grow on D-xylose and L-arabinose, the expression level of the integrated genes it was determined by measuring enzymatic activity. Isolates C25/AX1, C25/AX101, and C25/G8 were chosen for the enzymatic assays because they were the most stable integrants, as determined in the stability studies described below. The results of the enzymatic assays are summarized in Figures 14 and 15. For all assays (with and exception of xylulokinase), integrants showed positive activities as compared to the controls (C25 and/or 206C). It is believed, at this moment, that the low activity of XK for the integrants, might be due to experimental error, the nature of the assay, or both. In most assays, (excluding L-ribulokinase and xylose isomerase), the integrants showed lower activities than the plasmid-bearing strain (206C/pZB301). This is presumable related to the copy number of the genes.

For stability studies, the cultures were inoculated into test tubes containing RMG, incubated overnight at 30°C. and transferred daily to RMG tubes. The inoculum was controlled to allow transfer every 10 generations. At every 40 generations, the cells were used to inoculate

flasks, containing a mixture of sugars, to test the fermentation capabilities on the sugars without pH control at 30°C. Batch fermentation studies were performed at 30°C with pH control in Bio-StatQ chemostats, a trademark of B. Braun, Allentown, PA., using 500 ml as the working volume. The pH was automatically controlled with 2N KOH. Initial sugar concentration and pH
5 varied between each batch, depending on the culture conditions. All the sugars used were reagent grade. Samples were taken periodically throughout the fermentation, and analyzed for sugars, ethanol and by-products with HPLC, as described previously (Zhang 1995). Optical density, at 600 nm (OD600), was measured in order to monitor cell growth. Ethanol yield was based on the amount of total available sugar.

10 Several genomic integrated xylose and arabinose fermenting *Z. mobilis* strains developed through both homologous recombination and transposition were studied for their stability in a non-selective medium (RMG). These strains were cultured in RMG medium and serially transferred, daily, after about 10 generations. After every 40 generations, the cells were used to inoculate a flask containing 1% glucose and 2% xylose and 2% arabinose for examination of
15 their ability to ferment xylose and arabinose to ethanol. Ethanol process yields, and xylose and arabinose utilization rates, were used as the stability trait. Two of the isolates remained stable for 160 generations. See, Figures 16 and 17. Three integrated strains and a plasmid-bearing strain were further tested for fermentation performance, in a media containing a mixture of 4% glucose, 4% xylose, and 2% arabinose at pH 5.5 and 30°C. As shown in Figure 18, all three
20 strains utilized glucose, xylose and arabinose in 72 hours, while the plasmid-bearing strains still had 6 g/L residual arabinose. However, the integrated strains produced more xylitol (4 g/l) than the plasmid bearing strain (1 g/L). The two homologous recombination AX1 and AX101 strains did not produce lactate because the lactate dehydrogenase gene was inactivated through the gene integration. The process yields (about 83% of theoretical) of the integrated strains were very
25 similar to the plasmid bearing strain. Moreover, the integrated strains grew to a greater cell densities, which is probably due to a the lesser metabolic burden associated with having only singly copy of the seven genes.

While the present invention has been described in connection with the illustrated embodiments. It will be appreciated and understood that modifications may be made without
30 departing, from the true spirit and scope of the invention.

Claims

1. A transposon for stable insertion of foreign genes into a bacterial genome, comprising: at least one operon having structural genes encoding enzymes selected from the group consisting of *xylA**xylB*, *araBAD* and *tal/tkt*, and at least one promoter for expression of the structural genes in the bacterium, a pair of inverted insertion sequences, the operons contained
5 inside the insertion sequences, and a transposase gene located outside of the insertion sequences.

2. A plasmid vector containing the transposon of claim 1.

3. A bacterium transformed with the plasmid of claim 2.

4. The bacterium of claim 3 wherein the bacterium is *Z. mobilis*.

10 5. The bacterium of claim 3 wherein the transposon is a Tn5 or Tn10 derivative.

6. The bacterium of claim 4 wherein the operon includes the *xylA**xylB* and *tal/tkt* structural genes.

7. The bacterium of claim 4 wherein the operon includes the *araBAD* and *tal/tkt* structural genes.

15 8. The bacterium of claim 4 wherein the promoter is selected from the group consisting of *P_{eno}* and *P_{gap}*.

9. A plasmid vector for transformation of foreign genes into a bacterial genome, comprising: at least one operon having structural genes encoding enzymes selected from the group consisting of *xylA**xylB*, *araBAD* and *tal/tkt*, at least one promoter for expression of the structural genes in the bacterium, and at least two DNA fragments having homology with a DNA
20 sequence in the bacterial genome to be transformed.

10. A bacterium transformed with the vector of claim 9.

11. The bacterium of claim 6 further transformed with a plasmid vector including a second operon having structural genes encoding enzymes consisting essentially of *araBAD*, at least one promoter for expression of the structural genes in the bacterium, and at least two DNA fragments having homology with a DNA sequence in the bacterial genome to be transformed.
25

12. The bacterium of claim 7 further transformed with a plasmid vector including a second operon having structural genes encoding enzymes consisting essentially of *xylA**xylB*, at least one promoter for expression of the structural genes in the bacterium, and at least two DNA fragments having homology with a DNA sequence in the bacterial genome to be transformed.
30

13. The vector of claim 9 wherein the DNA fragments having homology are *ldhL* comprising a 2.5-Kb region of *Z. mobilis* DNA obtained as a template from a ATCC 39676 *Z. mobilis* strain.

14. The bacterium of claim 10 wherein the bacterium is *Z. mobilis*.

5 15. The bacterium of claim 6 wherein expression of a product of the structural gene is stable for at least 45 generations.

16. The bacterium of claim 11 wherein expression of a product of the structural gene is stable for at least 45 generations.

17. A vector pZB1862-*ldhL-ara* ATCC Accession No. PTA-1798.

10 18. A transposable element mini-Tn5-*tal/tkt-xylA* ATCC Accession No. PTA-1795.

19. A bacteria strain G8 ATCC Accession No. PTA-1796.

20. A bacteria strain C25 ATCC Accession No. PTA-1799.

21. A bacteria strain AX ATCC Accession No. PTA-1797.

15 22. A reaction mixture comprising a fermentable medium, the medium including xylose or arabinose and a bacterium as in any one of claims 3 to 8, 10 to 12, 14 to 16, or 19 to 21.

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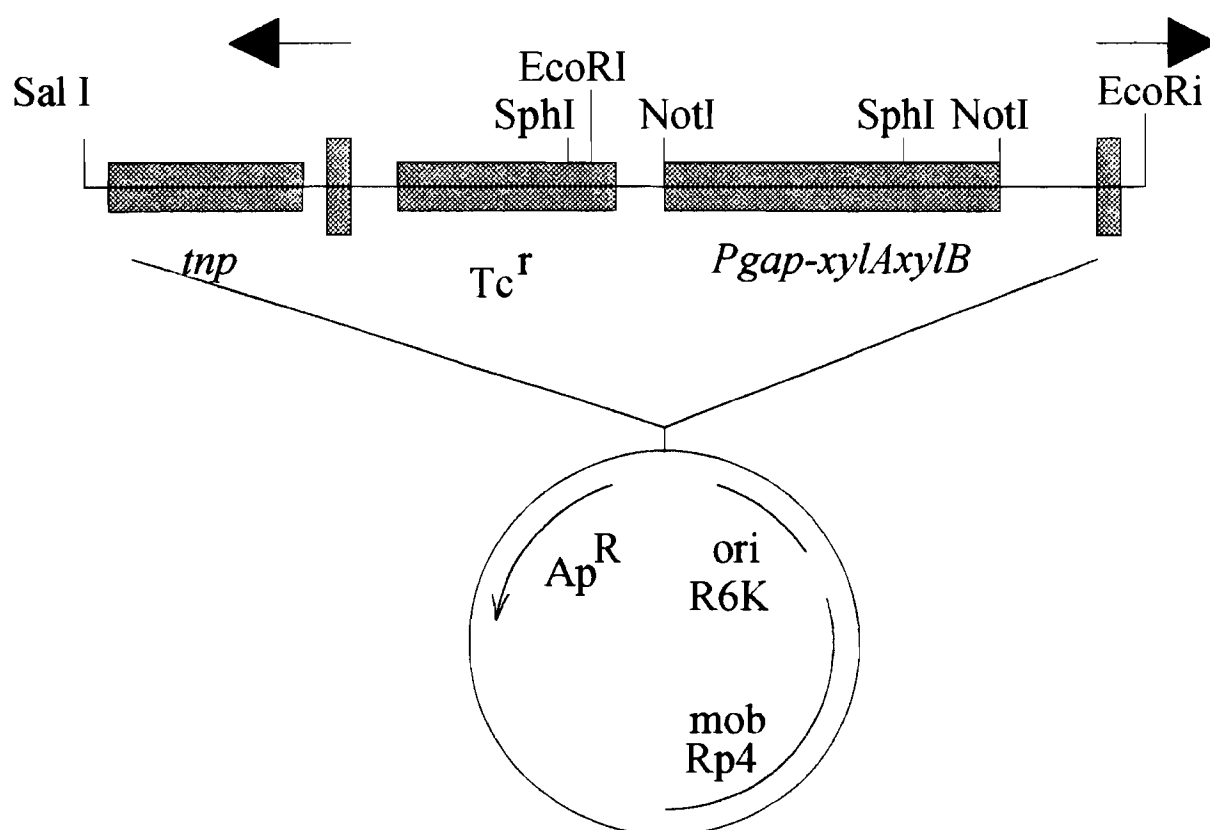


FIG. 1

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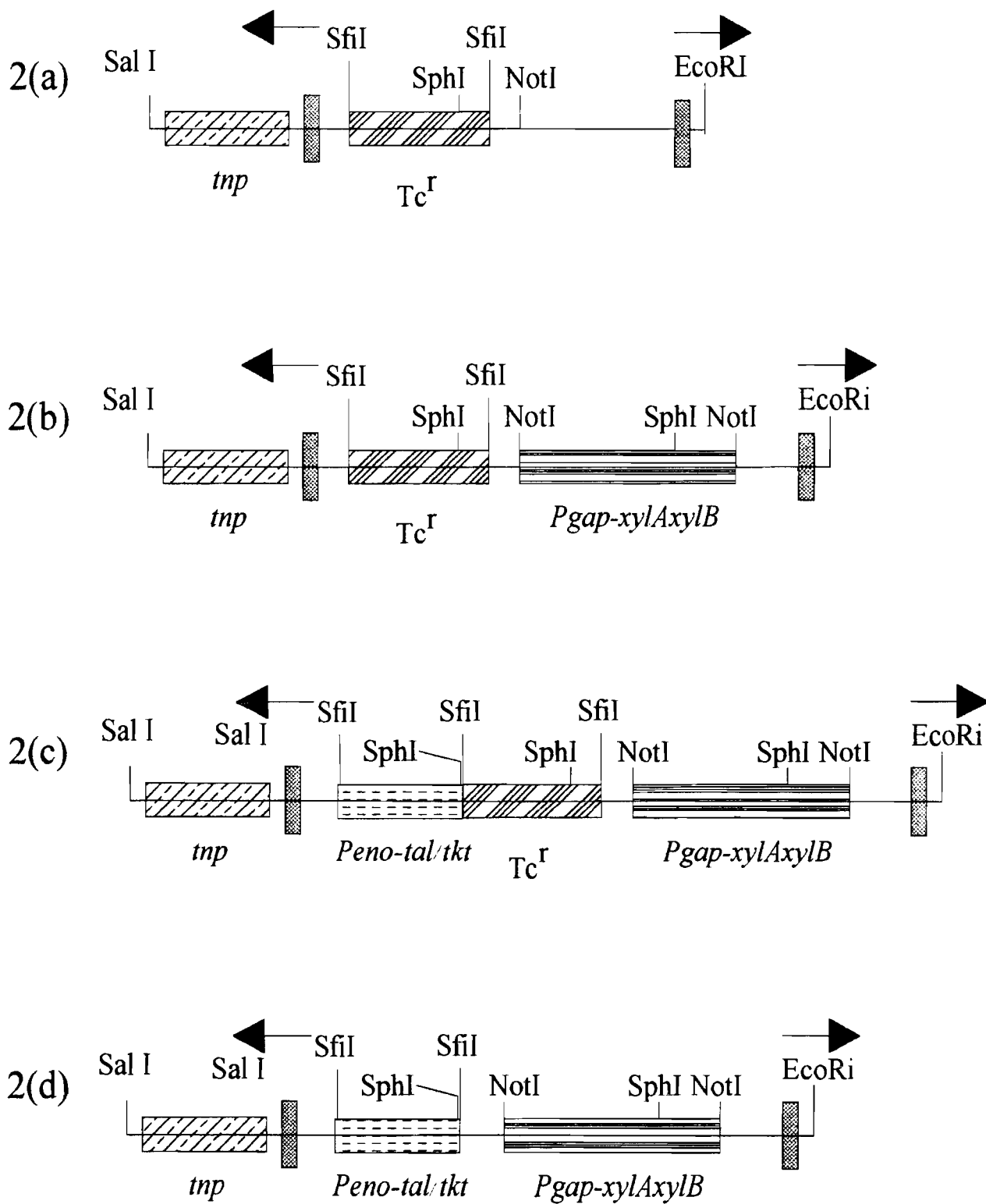


FIG. 2

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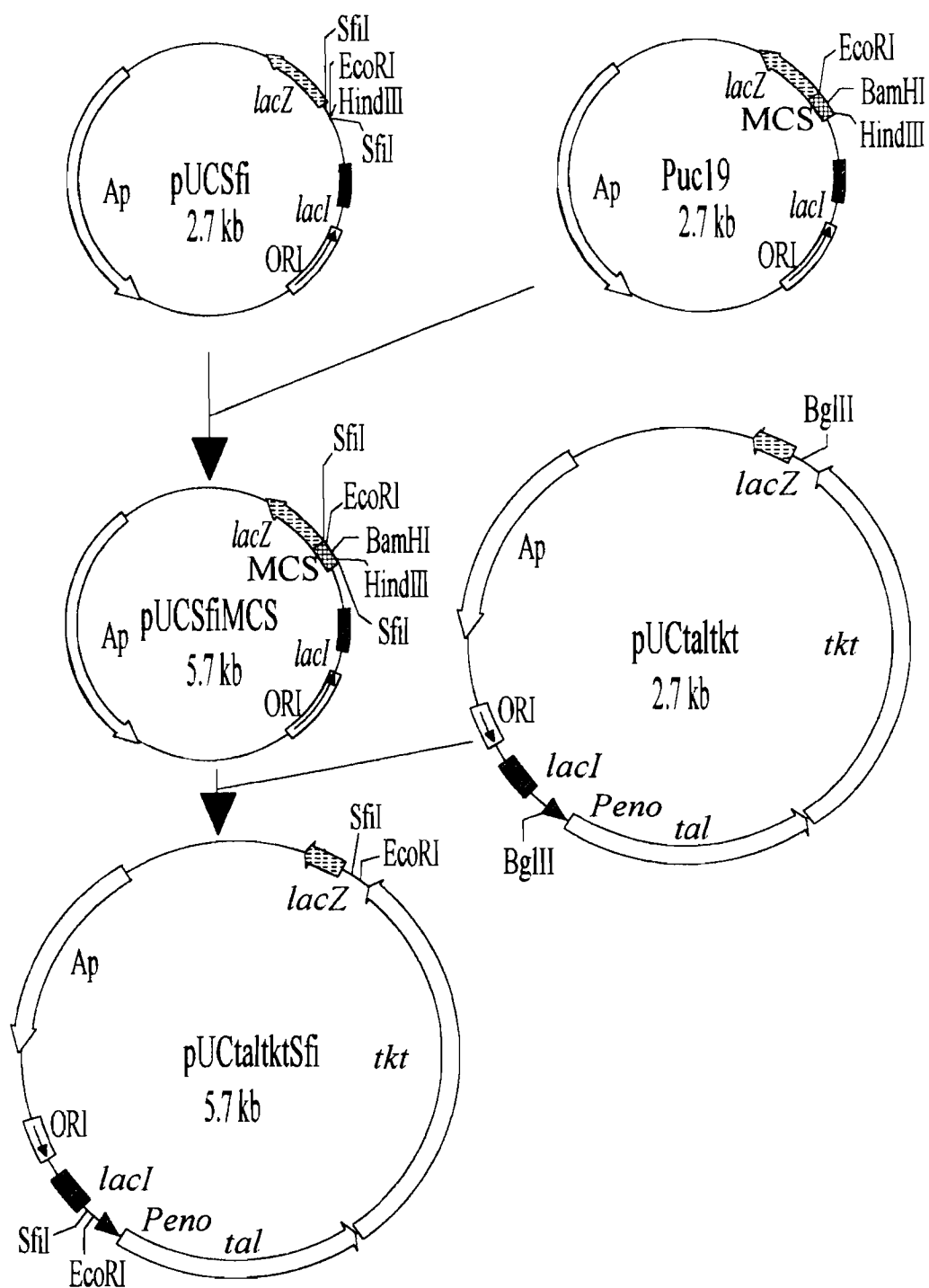


FIG. 4

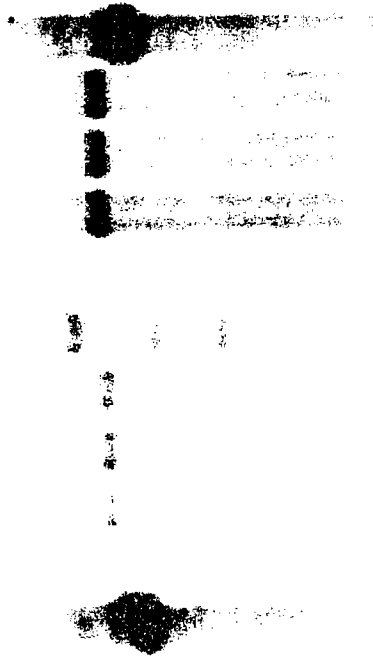


Figure 4

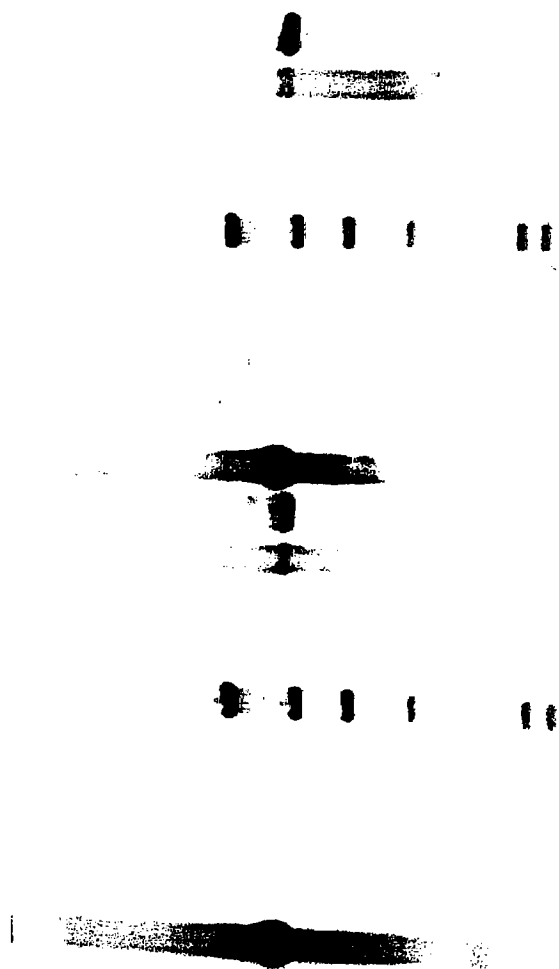


Figure 5

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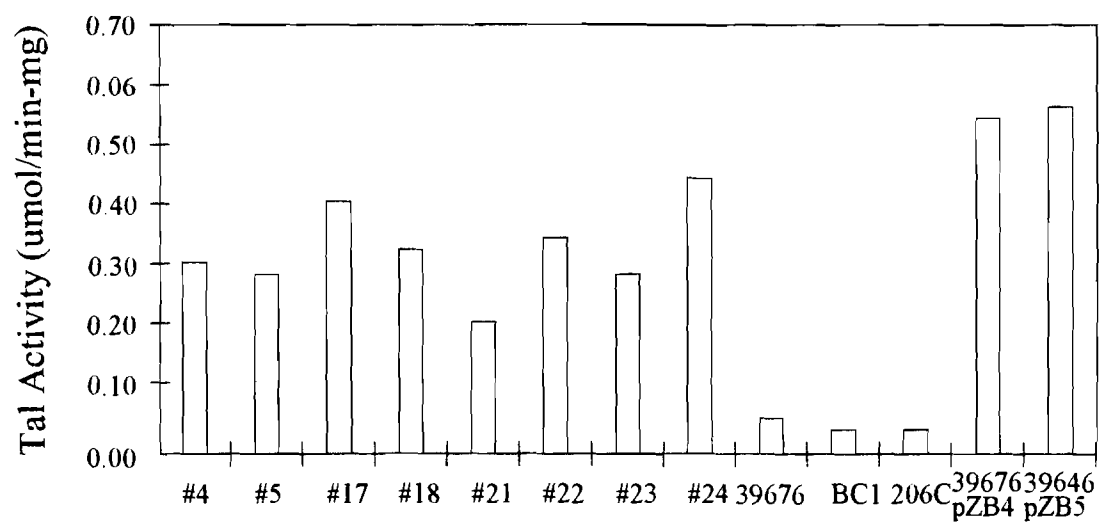
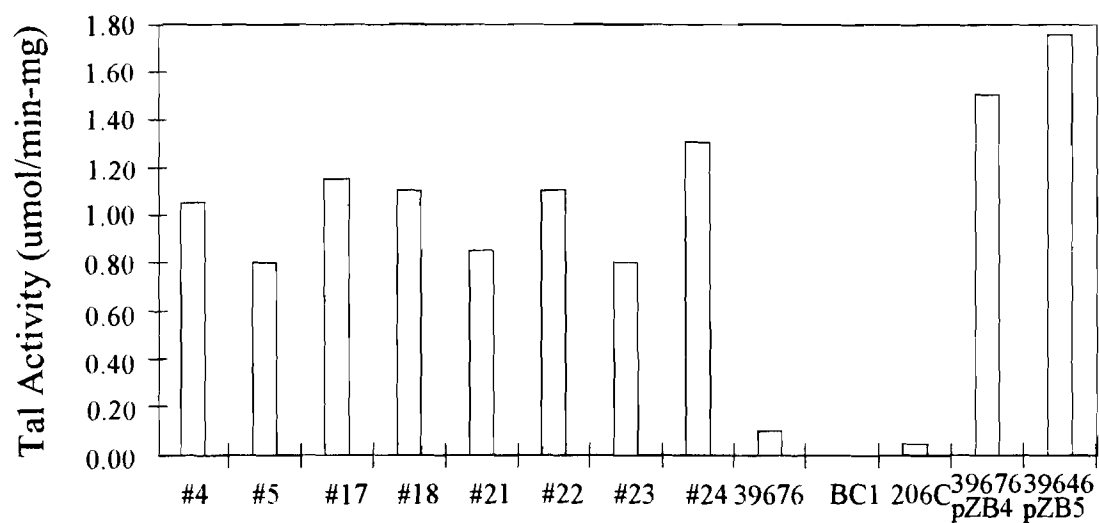
*Z. mobilis* Strains

FIG. 6

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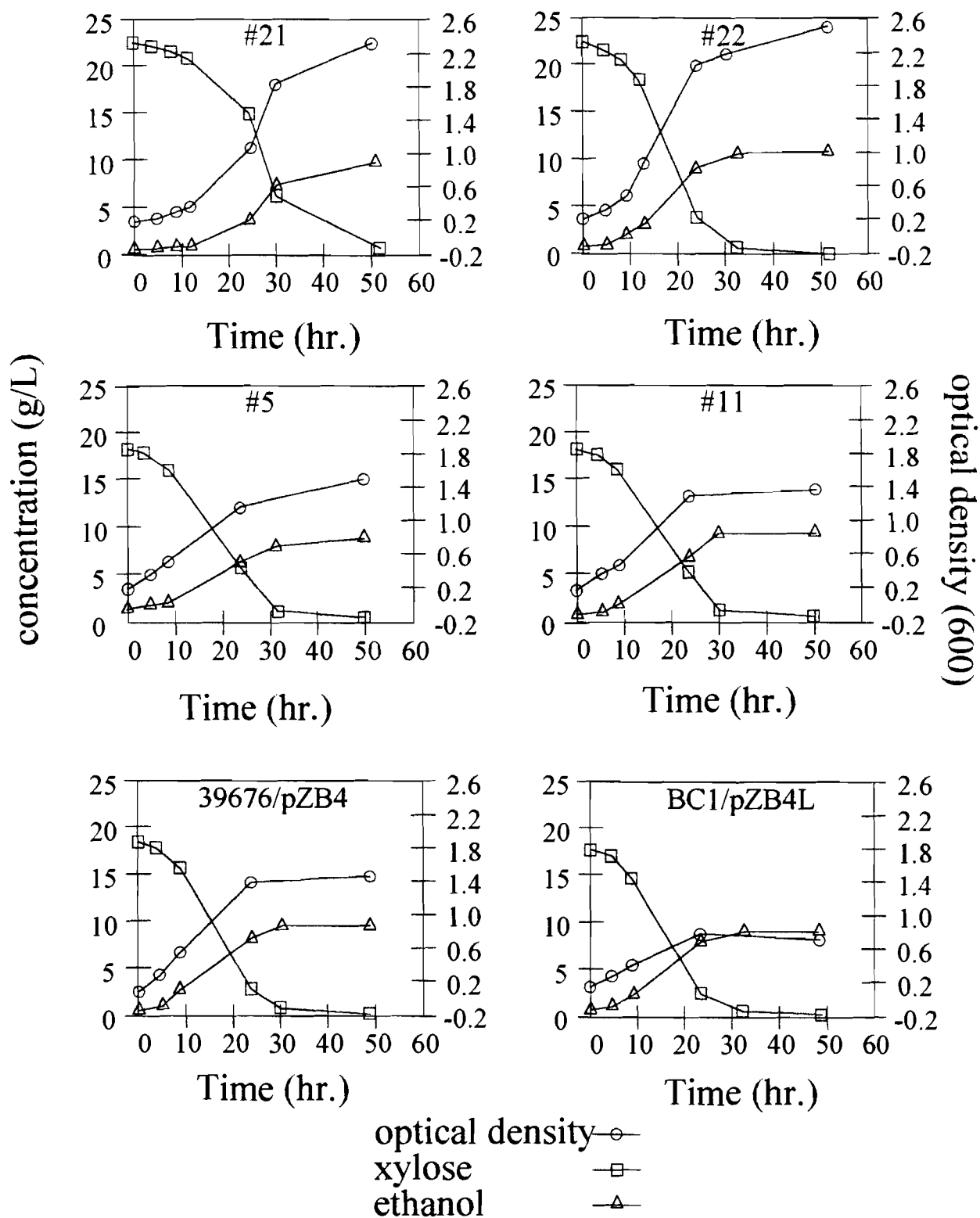


FIG. 7

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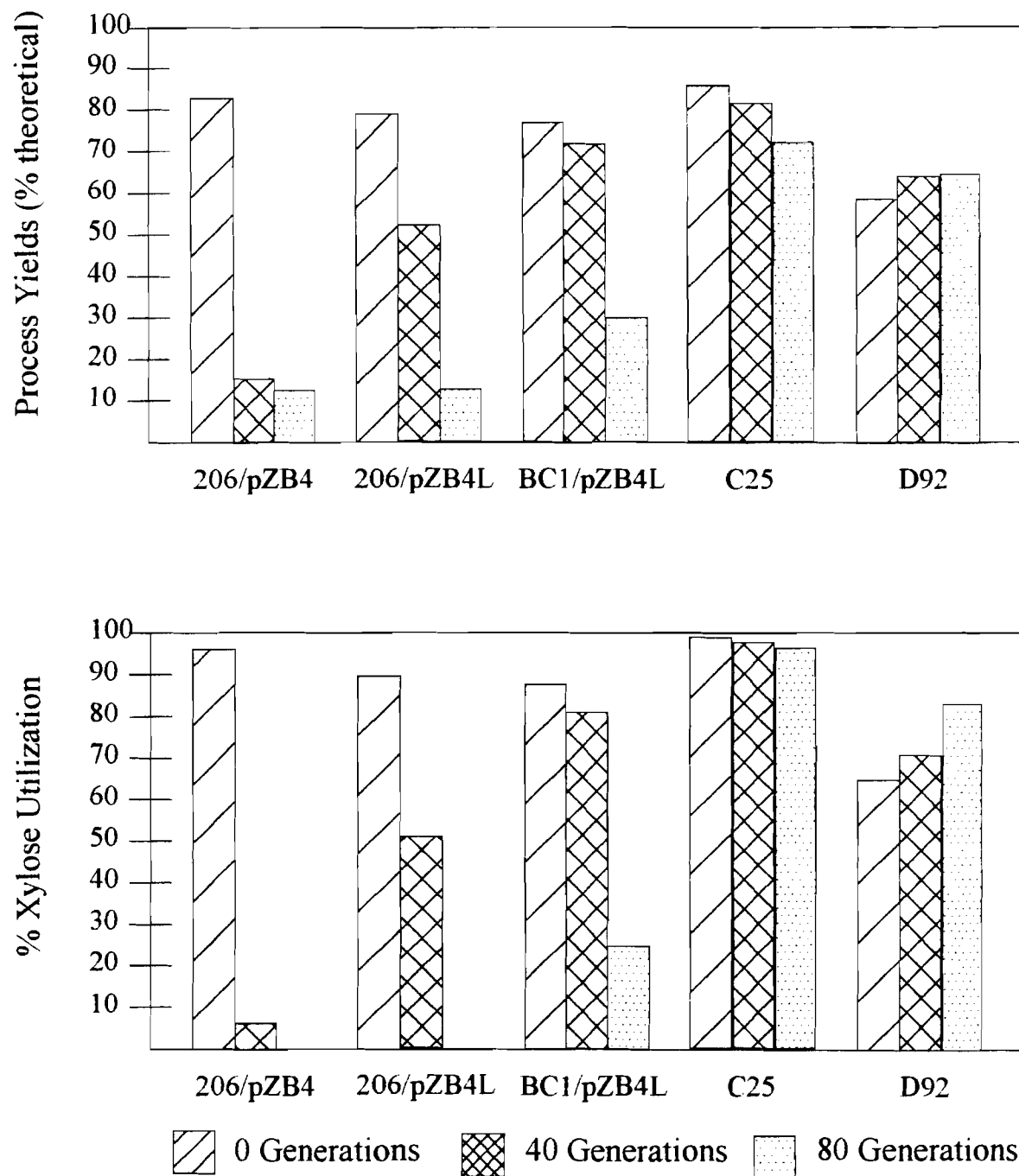


FIG. 8

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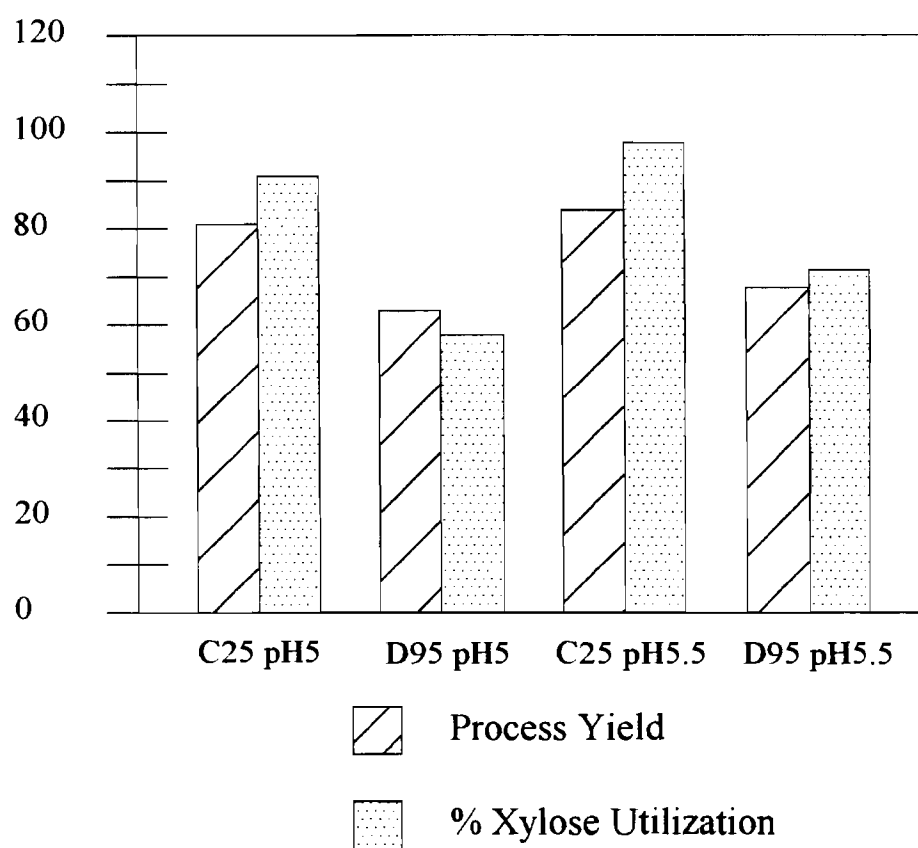


FIG. 9

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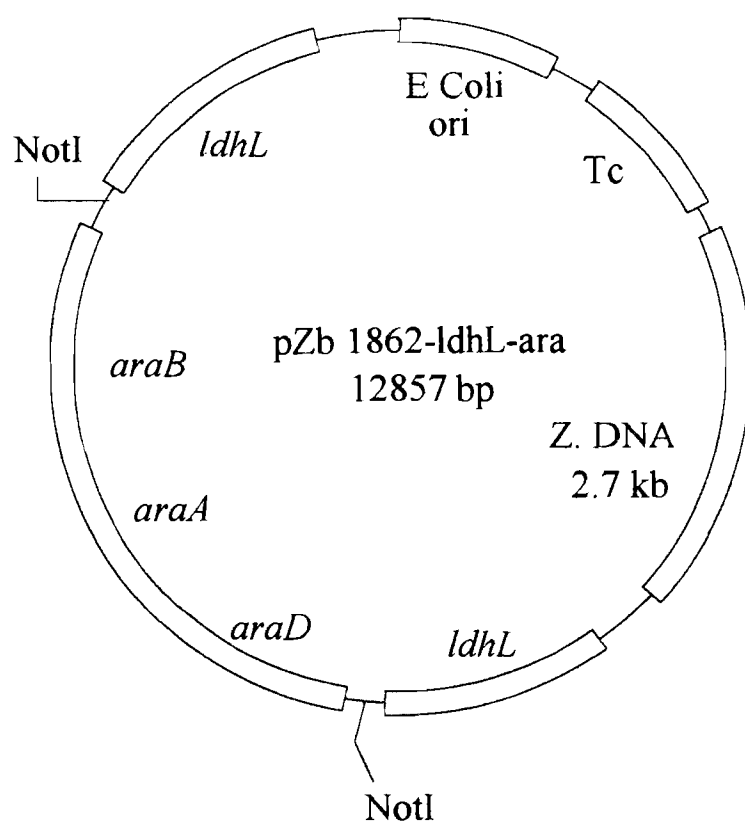


FIG. 10

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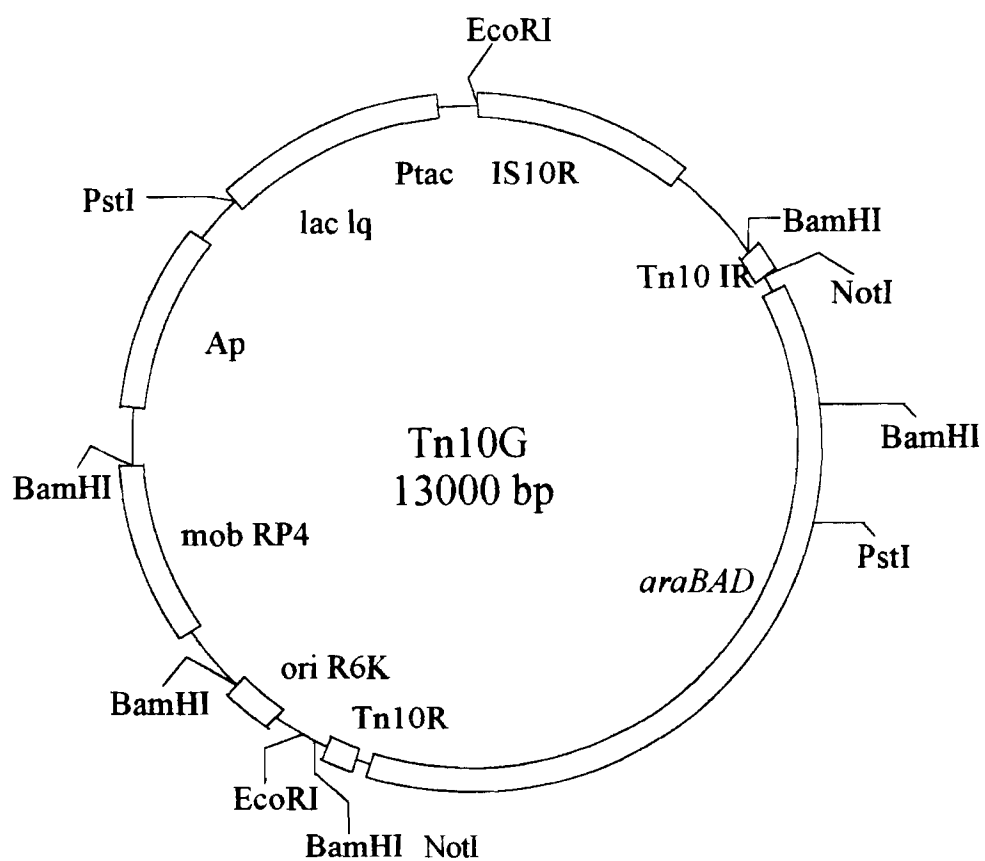


FIG. 11

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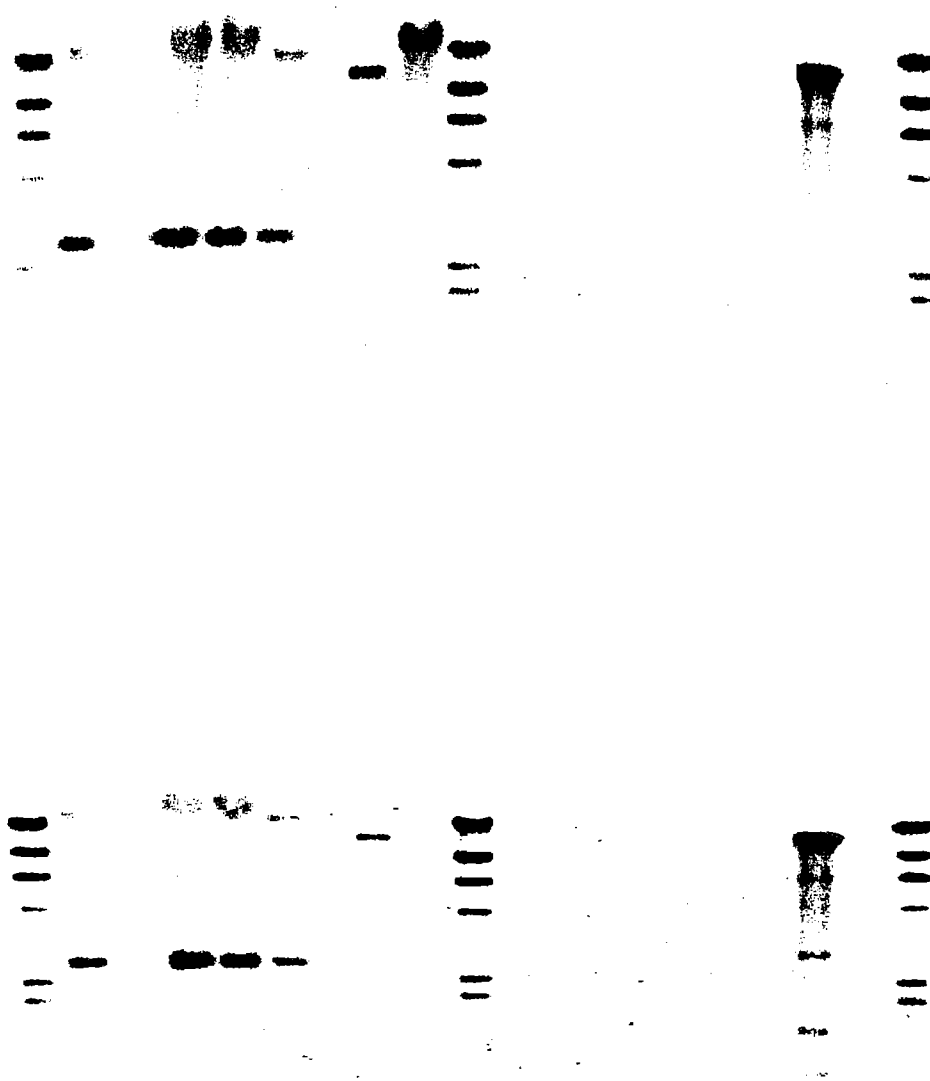


Figure 12

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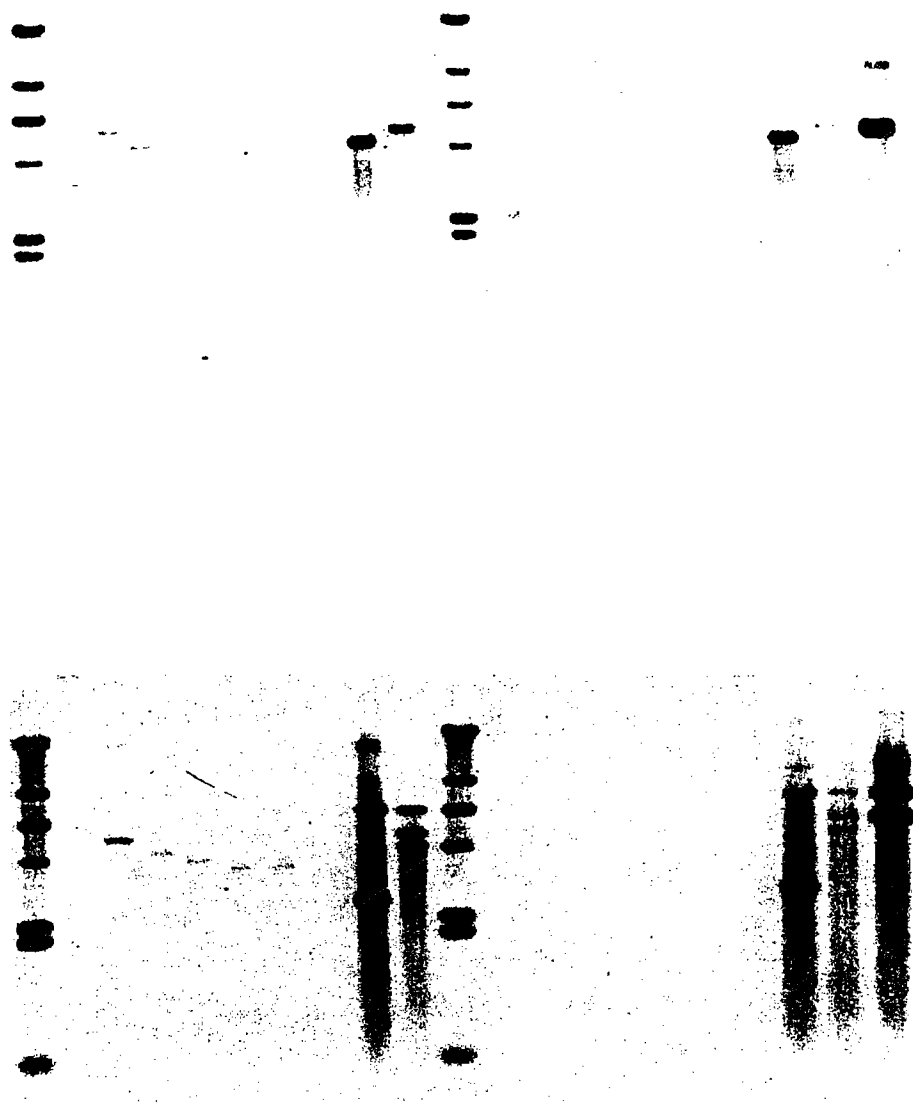


Figure 13

14/18

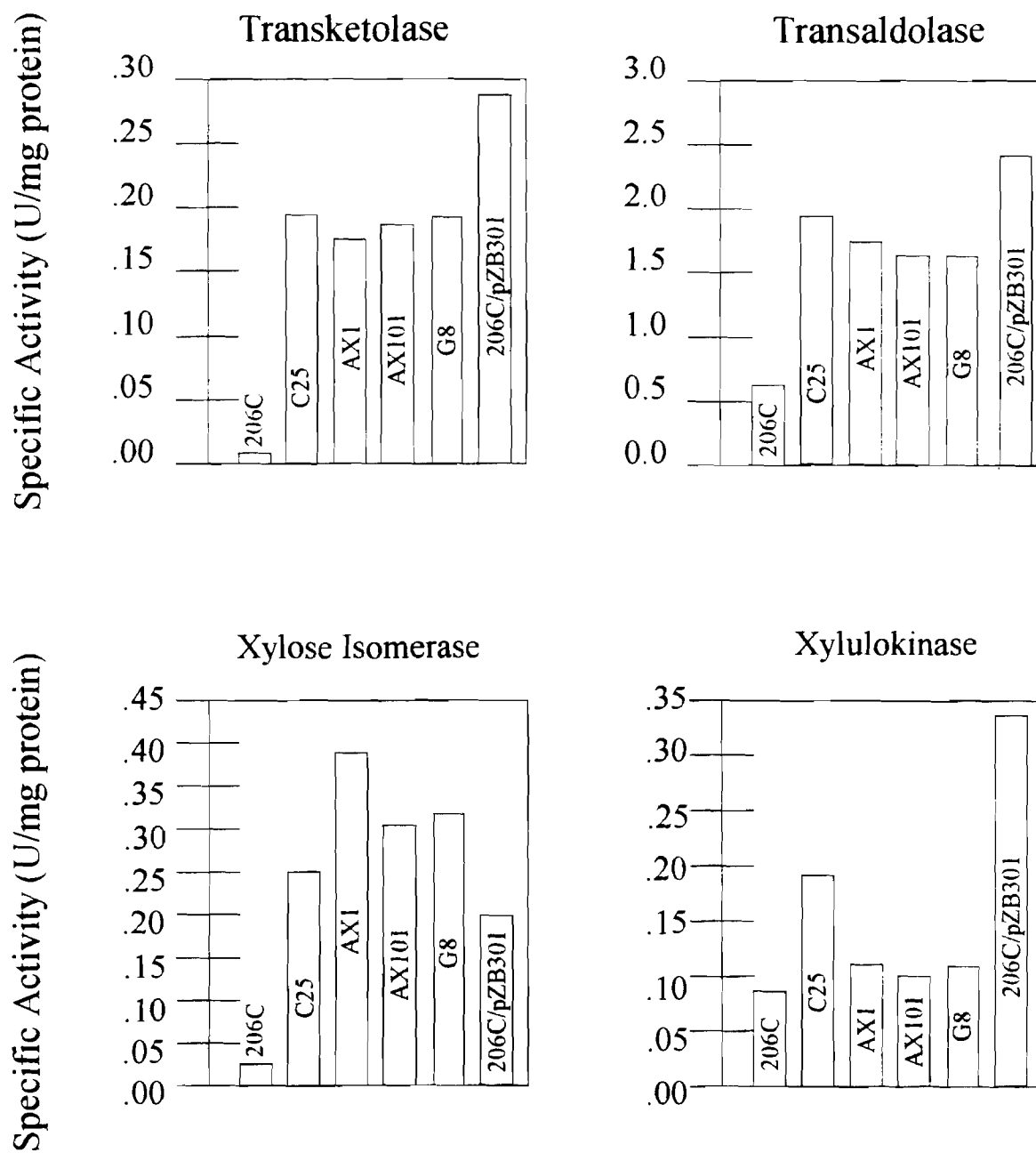
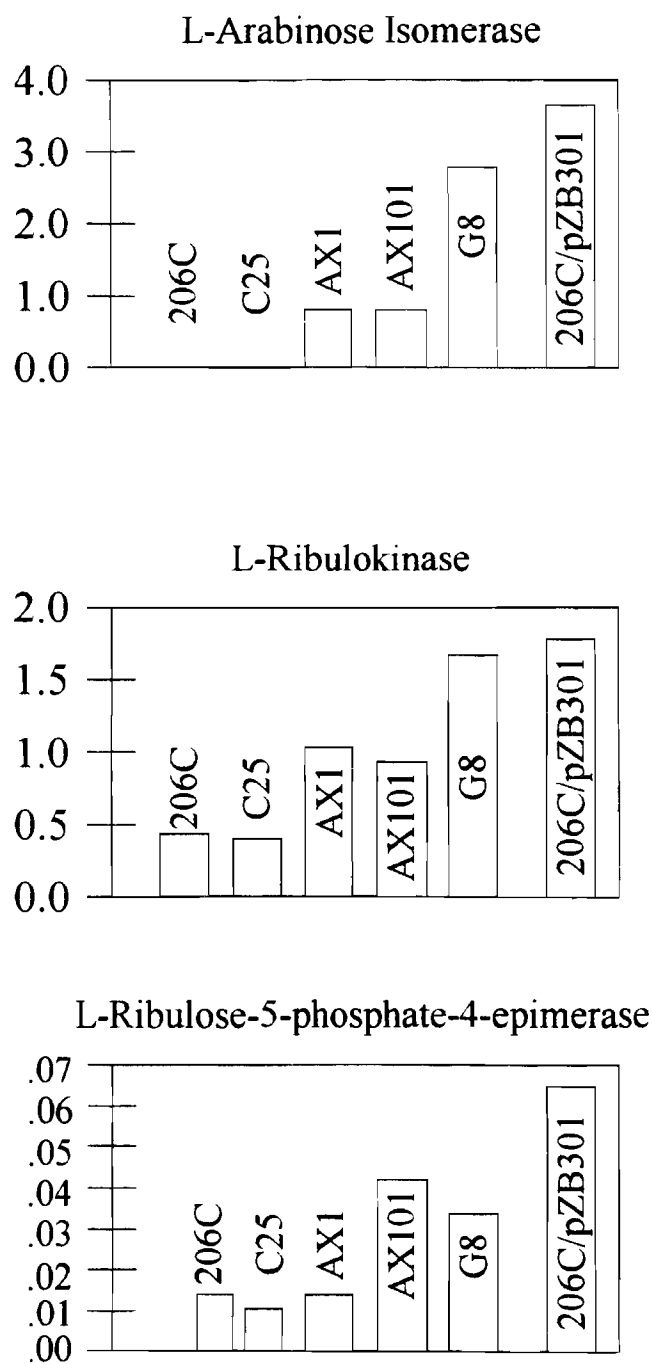


FIG. 14

15/18**FIG. 15**

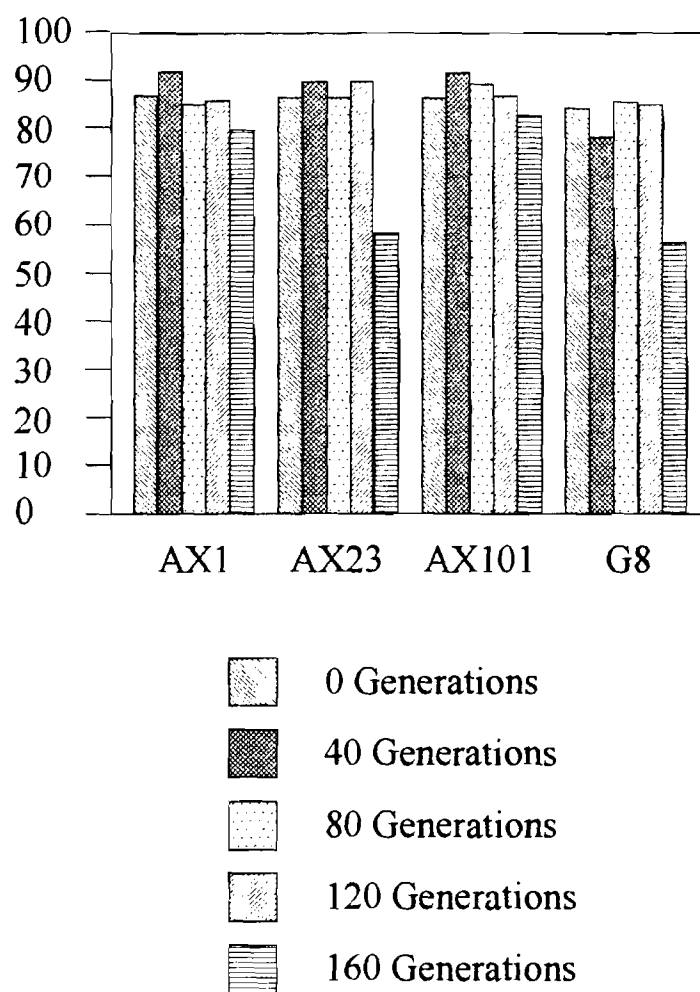
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FIG. 16

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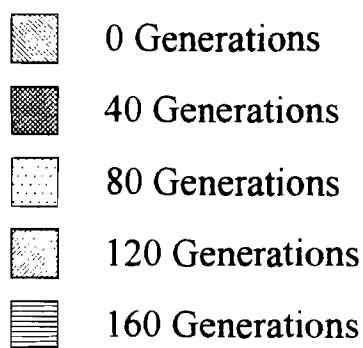
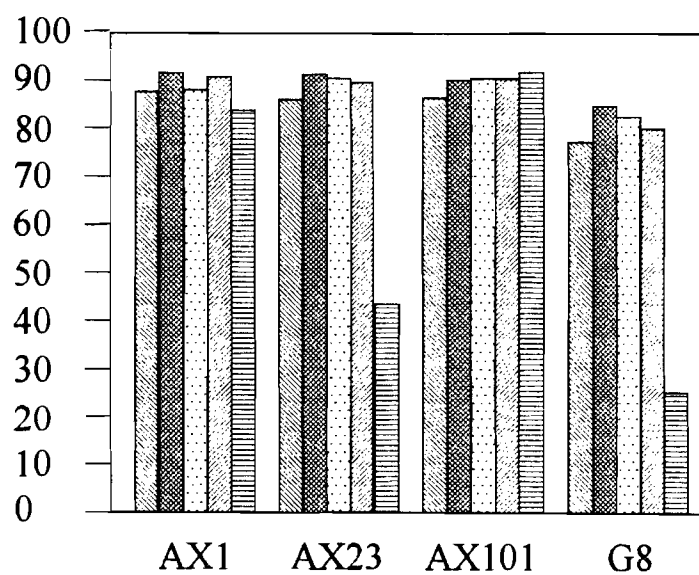
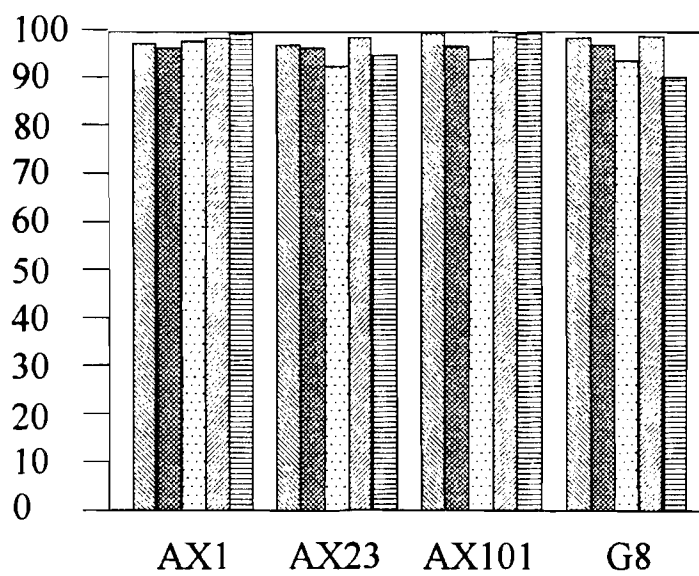


FIG. 17

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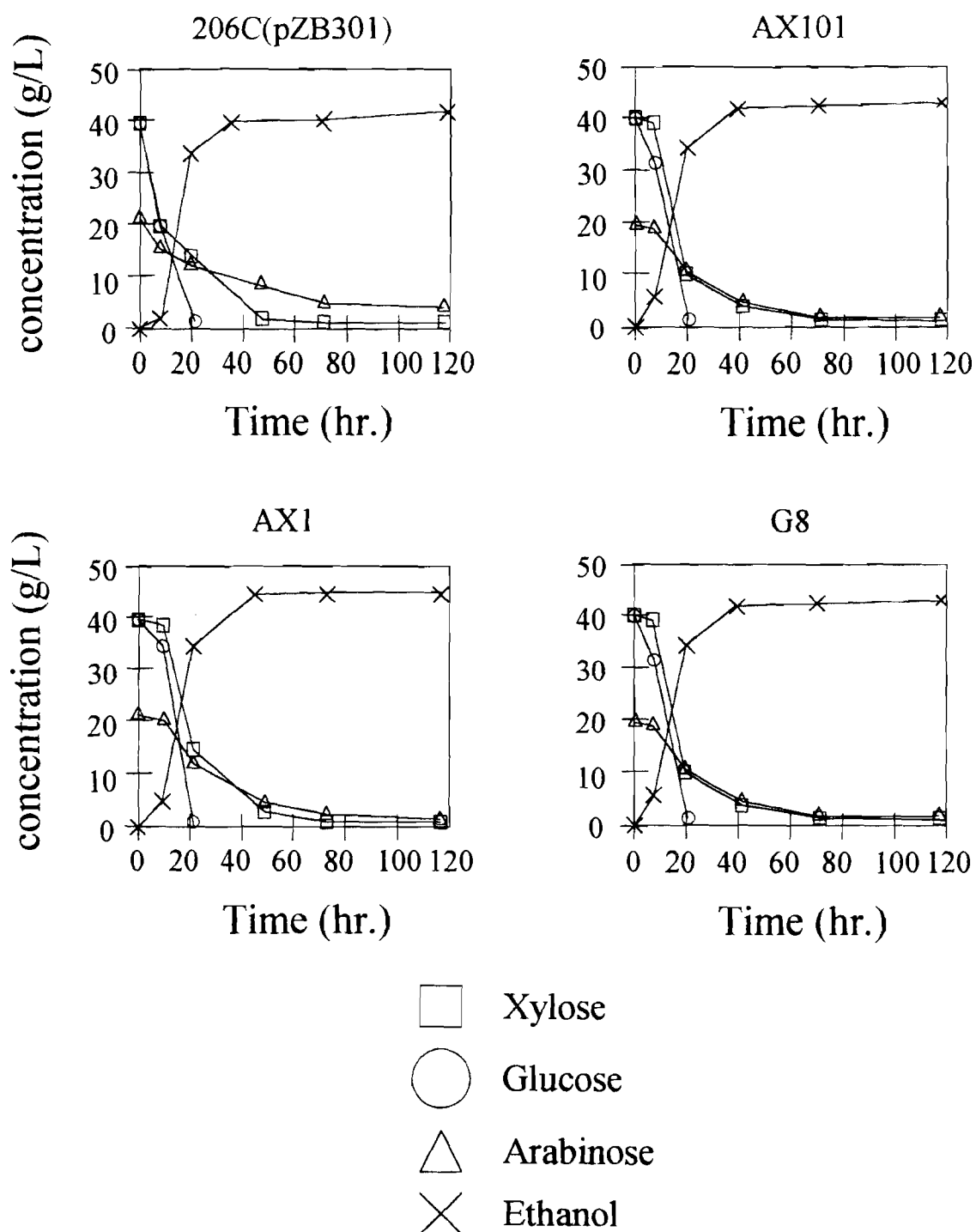


FIG. 18

SEQUENCE LISTING

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5 <120> STABLE ZYMOMONAS MOBILIS XYLOSE AND ARABINOSE
FERMENTING STRAINS

<130> PCT/00-14

10 <160> 16

<170> PatentIn Ver. 2.1

<210> 1

15 <211> 18

<212> DNA

<213> Artificial Sequence

<220>

20 <223> Description of Artificial Sequence: Tc primer for
DNA labeling

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18

25

<210> 2

<211> 18

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30 <213> Artificial Sequence

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<210> 3

10 <211> 20

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10 <223> Description of Artificial Sequence: Tnp primer for
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19

15

<210> 6

<211> 18

<212> DNA

20 <213> Artificial Sequence

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<213> Artificial Sequence

<220>

5 <223> Description of Artificial Sequence: Tal primer for
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<212> DNA

15 <213> Artificial Sequence

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<211> 45

<212> DNA

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amplification of ldhL gene fragment using PCR

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<212> DNA

<213> Artificial Sequence

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<220>

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using PCR

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<210> 16

<211> 24

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<223> Description of Artificial Sequence: Primer for
amplification of DIG labeled tnp gene fragment
using PCR

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24

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(43) International Publication Date
8 November 2001 (08.11.2001)

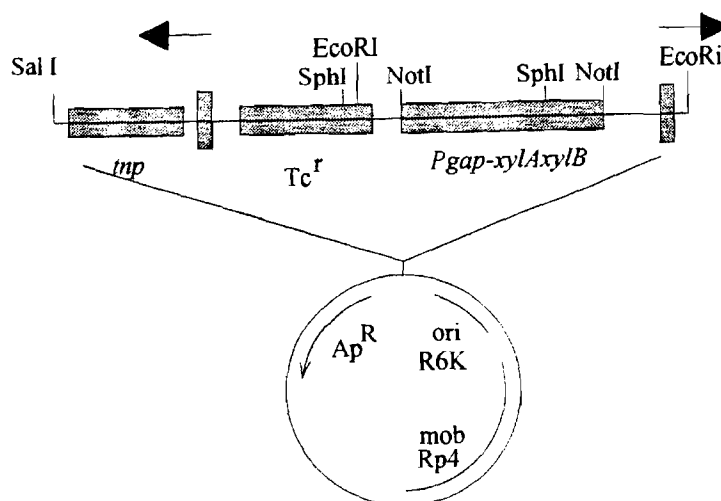
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- (71) Applicant: MIDWEST RESEARCH INSTITUTE
[US/US]; 425 Volker Boulevard, Kansas City, MO 64110 (US).
- (72) Inventors: ZHANG, Min; 14178 W. Warren Drive, Lakewood, CO 80228 (US). CHOU, Yat-Chen; 3641 Parfet Street, Wheatridge, CO 80033 (US).
- (74) Agent: WHITE, Paul, J.; National Renewable Energy Laboratory, 1617 Cole Boulevard, Golden, CO 80401 (US).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:
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- (88) Date of publication of the international search report:
20 June 2002

[Continued on next page]

(54) Title: STABLE *ZYMONOMAS MOBILIS* XYLOSE AND ARABINOSE FERMENTING STRAINS



(57) Abstract: The present invention briefly includes a transposon for stable insertion of foreign genes into a bacterial genome, comprising at least one operon having structural genes encoding enzymes selected from the group consisting of *xylAxyLB*, *araBAD* and *tal/tkt*, and at least one promoter for expression of the structural genes in the bacterium, a pair of inverted insertion sequences, the operons contained inside the insertion sequences, and a transposase gene located outside of the insertion sequences. A plasmid shuttle vector for transformation of foreign genes into a bacterial genome, comprising at least one operon having structural genes encoding enzymes selected from the group consisting of *xylAxyLB*, *araBAD* and *tal/tkt*, at least one promoter for expression of the structural genes in the bacterium, and at least two DNA fragments having homology with a gene in the bacterial genome to be transformed, is also provided. The transposon and shuttle vectors are useful in constructing significantly different *Zymomonas mobilis* strains, according to the present invention, which are useful in the conversion of the cellulose derived pentose sugars into fuels and



For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/11334

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/74 C12N15/90 C12N15/52 C12N1/21 C12P7/06

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, WPI Data, PAJ, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>"Improve Zymomonas for Xylose and Arabinose Fermentation"</p> <p>1998-99 OFFICE OF FUELS DEVELOPMENT PROJECT SUMMARIES, FERMENTATION ORGANISM DEVELOPMENT, 'Online!</p> <p>March 2000 (2000-03), XP002184798</p> <p>Retrieved from the Internet:</p> <p><URL: http://bioenergy.ornl.gov/99summaries/fermentation.html></p> <p>'retrieved on 2001-11-21!</p> <p>the whole document</p> <p style="text-align: center;">--- -/--</p>	1-22



Further documents are listed in the continuation of box C



Patent family members are listed in annex.

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Date of the actual completion of the international search

5 December 2001

Date of mailing of the international search report

22/01/2002

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
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Fax (+31-70) 340-2040

Authorized officer

Lejeune R

INTEI TIONAL SEARCH REPORT

Int onal Application No

PCT/US 01/11334

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category "	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CHOU Y C ET AL: "Inactivation of the D-lactate dehydrogenase gene in Zymomonas mobilis through homologous recombination." ABSTRACTS OF THE GENERAL MEETING OF THE AMERICAN SOCIETY FOR, vol. 99, 1999, page 370 XP002184799 99th General Meeting of the American Society for Microbiology; Chicago, Illinois, USA; May 30-June 3, 1999, 1999 ISSN: 1060-2011 the whole document	9,10,13, 14,22
A	WO 98 50524 A (MIDWEST RESEARCH INST) 12 November 1998 (1998-11-12) cited in the application the whole document	
A	WO 97 42307 A (CHEN ZHENG DAO ;HO NANCY W Y (US); PURDUE RESEARCH FOUNDATION (US)) 13 November 1997 (1997-11-13) the whole document	
A	ZHANG M ET AL: "GENETIC IMPROVEMENT OF Zymomonas mobilis FOR ETHANOL PRODUCTION: CHROMOSOMAL INTEGRATION OF THE XYLOSE- AND ARABINOSE-FERMENTING GENES" 22ND SYMPOSIUM ON BIOTECHNOLOGY FOR FUELS AND CHEMICALS, 7-10 MAY 2000, 'Online! 24 March 2000 (2000-03-24), XP002184800 Retrieved from the Internet: <URL:http://www.ct.ornl.gov/symposium/22nd/index_files/oral02.03.htm> 'retrieved on 2001-11-21! the whole document	1-22
A	PAPPAS K -M ET AL: "Transposon mutagenesis and strain construction in Zymomonas mobilis." JOURNAL OF APPLIED MICROBIOLOGY, vol. 82, no. 3, 1997, pages 379-388, XP001041553 ISSN: 1364-5072 cited in the application the whole document	
A	BEJAR S ET AL: "Construction of a new strain of Streptomyces violaceoniger, having strong, constitutive and stable glucose-isomerase activity." BIOTECHNOLOGY LETTERS, vol. 16, no. 12, 1994, pages 1259-1264, XP001041576 ISSN: 0141-5492 the whole document	

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/11334

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	LAWFORD HUGH G ET AL: "Fermentation performance assessment of a genomically integrated xylose-utilizing recombinant of <i>Zymomonas mobilis</i> 39676." APPLIED BIOCHEMISTRY AND BIOTECHNOLOGY, vol. 91-93, 1 April 2001 (2001-04-01), pages 117-131, XP001041535 ISSN: 0273-2289 the whole document	4-6,10, 14,15, 20,22
E,L	WO 01 83784 A (MIDWEST RES INST) 8 November 2001 (2001-11-08) the whole document L: priority	9,10,13, 14,17, 19,20,22

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/11334

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9850524	A	12-11-1998	US 5843760 A AU 7176898 A EP 1005530 A1 WO 9850524 A1	01-12-1998 27-11-1998 07-06-2000 12-11-1998
WO 9742307	A	13-11-1997	AU 731102 B2 AU 2830197 A BR 9710963 A EP 0898616 A1 JP 2000509988 T WO 9742307 A1	22-03-2001 26-11-1997 31-07-2001 03-03-1999 08-08-2000 13-11-1997
WO 0183784	A	08-11-2001	WO 0183784 A2	08-11-2001

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(21) International Application Number: PCT/US01/11334

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(30) Priority Data:
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2,304,929 2 May 2000 (02.05.2000) CA

(71) Applicant: MIDWEST RESEARCH INSTITUTE
[US/US]; 425 Volker Boulevard, Kansas City, MO 64110
(US).

(72) Inventors: ZHANG, Min; 14178 W. Warren Drive, Lake-
wood, CO 80228 (US). CHOU, Yat-Chen; 3641 Parfet
Street, Wheatridge, CO 80033 (US).

(74) Agent: WHITE, Paul, J.; National Renewable Energy
Laboratory, 1617 Cole Boulevard, Golden, CO 80401 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CH, CN, CO, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
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TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

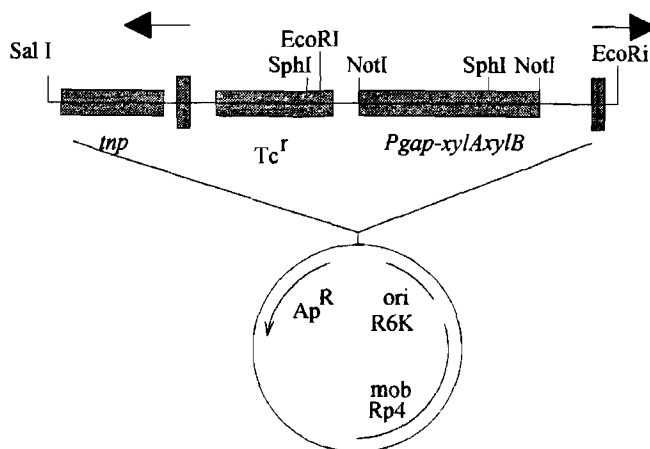
- with international search report
- with amended claims

(88) Date of publication of the international search report:
20 June 2002

Date of publication of the amended claims: 18 July 2002

[Continued on next page]

(54) Title: STABLE ZYMOMONAS MOBILIS XYLOSE AND ARABINOSE FERMENTING STRAINS



(57) Abstract: The present invention briefly includes a transposon for stable insertion of foreign genes into a bacterial genome, comprising at least one operon having structural genes encoding enzymes selected from the group consisting of *xylAxyB*, *araBAD* and *tal/tkt*, and at least one promoter for expression of the structural genes in the bacterium, a pair of inverted insertion sequences, the operons contained inside the insertion sequences, and a transposase gene located outside of the insertion sequences. A plasmid shuttle vector for transformation of foreign genes into a bacterial genome, comprising at least one operon having structural genes encoding enzymes selected from the group consisting of *xylAxyB*, *araBAD* and *tal/tkt*, at least one promoter for expression of the structural genes in the bacterium, and at least two DNA fragments having homology with a gene in the bacterial genome to be transformed, is also provided. The transposon and shuttle vectors are useful in constructing significantly different *Zymomonas mobilis* strains, according to the present invention, which are useful in the conversion of the cellulose derived pentose sugars into fuels and chemicals using traditional fermentation technology, because they are stable for expression in a non-selective medium.



For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

AMENDED CLAIMS

[received by the International Bureau on 15 March 2002 (15.03.02);
original claims 1-22 replaced by amended claims 1-19 (2 pages)]

1. A transposon for stable insertion of foreign genes into a bacterial genome, comprising: at least one operon having structural genes encoding enzymes selected from the group consisting of *xylA*/*xylB*, *araBAD* and *tal/tkt*, and at least one promoter for expression of the structural genes in the bacterium, a pair of inverted insertion sequences, the operons contained inside the insertion sequences, and a transposase gene located outside of the insertion sequences.
2. A plasmid vector containing the transposon of claim 1.
3. A bacterium transformed with the plasmid of claim 2.
4. The bacterium of claim 3 wherein the bacterium is *Z. mobilis*.
5. The bacterium of claim 3 wherein the transposon is a Tn5 or Tn10 derivative.
6. The bacterium of claim 4 wherein the operon includes the *xylA*/*xylB* and *tal/tkt* structural genes.
7. The bacterium of claim 4 wherein the operon includes the *araBAD* and *tal/tkt* structural genes.
8. The bacterium of claim 4 wherein the promoter is selected from the group consisting of *P_{eno}* and *P_{gap}*.
9. The bacterium of claim 6 further transformed with a plasmid vector including a second operon having structural genes encoding enzymes consisting essentially of *araBAD*, at least one promoter for expression of the structural genes in the bacterium, and at least two DNA fragments having homology with a DNA sequence in the bacterial genome to be transformed.
10. The bacterium, of claim 7 further transformed with a plasmid vector including a second operon having structural genes encoding enzymes consisting essentially of *xylA*/*xylB*, at least one promoter for expression of the structural genes in the bacterium, and at least two DNA fragments having

homology with a DNA sequence in the bacterial genome to be transformed.

11. The bacterium of claim 6 wherein expression of a product of the structural gene is stable for at least 45 generations.

12. The bacterium of claim 9 wherein expression of a product of the structural gene is stable for at least 45 generations.

13. A vector pZB1862-ldhL-ara, ATCC Accession No. PTA-1798.

14. A transposable element mini-Tn5-*tal/tkt-xyIaxylB*, ATCC Accession No. PTA-1795

15. A bacteria strain G8, ATCC Accession No. PTA-1796.

16. A bacteria strain C2,5 ATCC Accession No. PTA-1799.

17. A bacteria strain AX, ATCC Accession No. PTA-1797.

18. A reaction mixture comprising a fermentable medium, the medium including xylose or arabinose and a bacterium as in any one of claims 3 to 8, 9, 10, 11, 12, 14-16, or 18.

19. The bacterium of claim 3 wherein the bacterium is *Zymomonas*.